

SEQ ID	Model	Description	E-value	Score	Repeats	Position
						344:345-374:375-407
1701	URO-D	Uroporphyrinogen decarboxylase (URO-D)	7.8	-229.7	1	79-354
1702	pkinase	Protein kinase domain	0.00012	-68.0	1	31-278
1702	HEAT	HEAT repeat	1.2	15.6	2	342-380:499-537
1705	cyclin	Cyclin, N-terminal domain	3.8e-11	50.5	1	157-279
1708	WD40	WD domain, G-beta repeat	1.5e-11	51.8	5	278-313:371-407:413-447:493-529:535-569
1709	SH2	SH2 domain	0.002	10.0	1	287-364
1710	abhydrolase	alpha/beta hydrolase fold	2.2e-20	81.2	1	124-355
1710	abhydrolase_2	Phospholipase/Carboxylesterase	1.2	-84.9	1	179-359
1711	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.002	23.7	1	280-320
1711	PHD	PHD-finger	1.9	-12.4	1	282-323
1712	WD40	WD domain, G-beta repeat	3.2e-18	74.0	5	67-101:123-157:164-199:209-246:253-290
1714	Acyltransferase	Acyltransferase	0.0011	14.0	1	83-217
1719	helicase_C	Helicase conserved C-terminal domain	1.2e-19	78.7	1	397-475
1719	DEAD	DEAD/DEAH box helicase	4.6e-07	10.4	1	2-210
1719	IPT	Isopentenyl transferase	7.9	-160.7	1	17-172
1720	Na_Ca_Ex	Sodium/calcium exchanger protein	8e-76	265.3	2	109-249:471-616
1720	DUF205	Domain of unknown function DUF	5.3	-112.7	1	85-253
1720	Fumarate_red_D	Fumarate reductase subunit D	8.4	-49.5	1	518-620
1721	vwa	von Willebrand factor type A domain	9.6e-29	108.9	1	34-205
1721	fn3	Fibronectin type III domain	3e-15	64.1	2	212-287:332-413
1724	pkinase	Protein kinase domain	1.6e-06	-41.3	1	40-359
1725	BRCT	BRCA1 C Terminus (BRCT) domain	1e-15	65.6	3	3-93:642-730:753-833
1727	BRCT	BRCA1 C Terminus (BRCT) domain	7.2	1.2	1	45-130
1728	rrm	RNA recognition motif.	1.1e-05	32.4	2	545-612:880-942
1728	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H type	0.012	22.2	1	285-311
1728	PWI	PWI domain	0.047	-0.6	1	6-78
1730	PX	PX domain	2.5e-31	117.5	1	94-211
1731	PMP22_Claudin	PMP-22/EMP/MP20/Claudin family	1.5e-56	201.3	1	1-157

SEQ ID	Model	Description	E-value	Score	Repeats	Position
1733	homeobox	Homeobox domain	0.00037	21.6	1	268-339
1733	Vac_Fusion	Chordopoxvirus fusion protein	5.2	-21.5	1	286-364
1733	CUT	CUT domain	8.5	-38.0	1	159-240
1734	homeobox	Homeobox domain	0.00037	21.6	1	268-339
1734	Vac_Fusion	Chordopoxvirus fusion protein	5.2	-21.5	1	286-364
1734	CUT	CUT domain	8.5	-38.0	1	159-240
1738	efhand	EF hand	1.5e-16	68.4	2	40-68:76-104
1742	trypsin	Trypsin	6.5	-55.6	1	33-255
1743	Exonuclease	Exonuclease	1.2e-36	135.2	1	39-213
1745	Smr	Smr domain	0.0029	13.0	1	1594-1672
1745	RyR	RyR domain	1.5	-29.0	1	1312-1403
1745	L27	L27 domain	3.6	5.1	1	1573-1626
1746	Smr	Smr domain	0.0029	13.0	1	1611-1689
1746	RyR	RyR domain	1.5	-29.0	1	1312-1403
1746	L27	L27 domain	3.6	5.1	1	1590-1643
1746	Smg4_UPF3	Smg-4/UPF3 family	9.7	-74.5	1	1379-1518
1747	mito_carr	Mitochondrial carrier protein	1.3e-81	284.5	3	1-90:98-198:200-288
1748	OSCP	ATP synthase delta (OSCP) subunit	8.4	-94.4	1	67-213
1749	Oxysterol BP	Oxysterol-binding protein	3.4e-78	273.2	1	488-875
1749	PH	PH domain	2.2e-09	44.6	1	52-146
1750	lactamase B	Metallo-beta-lactamase superfamily	4.1	-28.9	1	1-153
1751	lipoxxygenase	Lipoxygenase	9.5e-133	454.4	1	126-703
1751	PLAT	PLAT/LH2 domain	1.6e-33	124.8	1	2-116
1753	Rho_GDI	RHO protein GDP dissociation inhibitor	3.2e-113	389.5	1	1-187
1756	GRAM	GRAM domain	7.5e-17	69.4	1	110-177
1757	homeobox	Homeobox domain	3.6e-29	110.3	1	21-77
1758	lipocalin	Lipocalin / cytosolic fatty-acid binding protein	1.1e-24	95.4	1	38-168
1759	ig	Immunoglobulin domain	3.1e-13	57.4	2	35-112:160-234
1761	oxidored_q1	NADH-Ubiquinone/plastoquinone (complex I)	0.078	-128.7	1	16-259
1761	DUF250	Domain of unknown function, DUF250	0.45	-85.1	1	162-337
1761	DUF6	Integral membrane protein DUF6	2.5	-14.8	1	192-328
1761	secY	eubacterial secY protein	7.2	-246.6	1	36-243
1761	FecCD	FecCD transport family	9.8	-221.2	1	120-328
1762	Keratin_B2	Keratin, high sulfur B2 protein	3.3e-07	32.9	2	11-113:114-204
1763	sugar_tr	Sugar (and other) transporter	0.018	-119.2	1	43-449
1763	oxidored_q1	NADH-Ubiquinone/plastoquinone (complex I)	4.7	-165.1	1	146-442
1765	VPS9	Vacuolar sorting protein 9 (VPS9) domain	4.5e-33	123.3	1	380-484
1765	RA	Ras association (RalGDS/AF-6) domain	0.73	-5.9	1	518-607

SEQ ID	Model	Description	E-value	Score	Repeats	Position
1766	SSF	Sodium:solute symporter family	5.9e-206	697.6	1	106-535
1766	oxidored_q1	NADH-Ubiquinone/plastoquinone (complex I)	4.8	-165.2	1	216-521
1766	MIP	Major intrinsic protein	5.8	-121.9	1	112-364
1766	DsbD	Cytochrome C biogenesis protein transmemb	8.6	-97.3	1	195-425
1767	Peptidase M3	Peptidase family M3	1.3e-203	689.8	1	251-701
1768	RasGAP	GTPase-activator protein for Ras-like	1.3e-26	101.9	1	449-621
1768	PH	PH domain	0.012	22.2	1	112-236
1768	C2	C2 domain	2.6	-10.9	1	249-332
1768	Tymo_45 kd_70kd	Tymovirus 45/70Kd protein	4.2	-293.9	1	561-979
1768	RNA_pol	DNA-dependent RNA polymerase	5.1	-234.7	1	381-1225
1768	PHD	PHD-finger	6.9	-17.6	1	214-273
1770	rrm	RNA recognition motif.	0.48	5.6	2	238-323:352-422
1772	zf-C2H2	Zinc finger, C2H2 type	1.6e-87	304.2	13	49-71:197-219:225-247:253-275:281-303:309-331:337-359:365-387:393-415:421-443:449-471:477-499:505-527
1772	zf-BED	BED zinc finger	8.9	-6.9	1	490-528
1773	ATP-synt_C	ATP synthase subunit C	5.4e-08	40.0	1	62-127
1774	zf-B_box	B-box zinc finger	7.2e-14	59.5	1	90-131
1774	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	1.6e-10	48.4	1	15-58
1774	PHD	PHD-finger	1.1	-10.3	1	14-61
1774	zf-AN1	AN1-like Zinc finger	1.4	-3.2	1	15-53
1774	zf-UBR1	Putative zinc finger in N-recogin	7.6	-23.6	1	93-146
1775	FH2	Formin Homology 2 Domain	5.4e-50	179.5	1	21-455
1775	WH2	WH2 motif	0.0058	23.3	1	441-456
1777	PHD	PHD-finger	8.7	-18.6	1	493-522
1779	Branch	Core-2/I-Branching enzyme	3.9e-05	-52.8	1	175-516
1780	TFIIS	Transcription factor S-II (TFIIS)	3.9	-3.7	1	295-344
1781	SH3	SH3 domain	1.3e-13	58.6	1	454-508
1782	filament	Intermediate filament protein	3.9	-200.0	1	134-406
1783	SET	SET domain	2e-53	190.9	1	3878-4006
1783	PHD	PHD-finger	4.7e-28	106.6	3	20-71:72-118:147-200
1783	HMG_box	HMG (high mobility group) box	0.0047	12.3	1	710-773
1783	DC1	DC1 domain	8.5	1.7	3	19-50:69-98:146-176
1784	zf-DHHC	DHHC zinc finger domain	2.4e-25	97.7	1	90-154
1785	zf-C2H2	Zinc finger, C2H2 type	9.3e-14	59.1	4	18-40:64-86:92-

SEQ ID	Model	Description	E-value	Score	Repeats	Position
						115:178-200
1788	ion_trans	Ion transport protein	8.3e-18	72.6	1	438-672
1788	ank	Ankyrin repeat	1.9e-06	34.8	2	77-108:163-195
1788	Srg	C.elegans Srg family integral membrane prot	8.1	-222.4	1	418-669
1791	ubiquitin	Ubiquitin family	0.0036	24.0	1	124-195
1792	Gag_p10	Retroviral GAG p10 protein	4e-23	90.2	1	1-89
1798	Ribosomal S12	Ribosomal protein S12	0.003	-14.2	1	7-66
1799	efhand	EF hand	1.1e-07	39.0	3	281-309:318-346:353-381
1799	Acyltransferase	Acyltransferase	0.0001	26.8	1	18-203
1801	zf-C2H2	Zinc finger, C2H2 type	3.2e-79	276.6	12	160-182:188-210:216-238:244-266:272-294:300-322:355-377:431-453:459-481:487-509:515-537:543-565
1801	LIM	LIM domain	4.7	-17.4	1	433-487
1802	lectin_c	Lectin C-type domain	1.4e-25	98.4	1	143-250
1802	lectin_c	Lectin C-type domain	1.4e-25	98.4	1	143-250
1804	efhand	EF hand	2.5e-08	41.1	2	16-44:56-82
1806	LRR	Leucine Rich Repeat	1.5e-07	38.5	5	130-151:152-173:174-195:196-217:221-243
1807	COX3	Cytochrome c oxidase subunit III	3.5	-233.2	1	51-219
1807	CbiM	CbiM	9.2	-93.3	1	114-249
1807	oxidored_q5_N	NADH-ubiquinone oxidoreductase chain 4	9.8	-59.5	1	89-169
1808	Sulfotransfer	Sulfotransferase protein	6.6	-108.5	1	39-282
1814	Metallophos	Calcineurin-like phosphoesterase	0.23	14.3	1	36-241
1815	rrm	RNA recognition motif	0.67	4.1	1	201-269
1816	filament	Intermediate filament protein	1.5	-188.9	1	1-253
1817	MAGE	MAGE family	4.2e-17	70.3	2	14-613:655-867
1817	Atrophin-1	Atrophin-1 family	9.5	-684.8	1	4-783
1818	Tropomod	Tropomodulin	8.1	-168.0	1	362-653

SEQ ID	Model	Description	E-value	Score	Repeats	Position
	ulin					
1819	Hydrolase	haloacid dehalogenase-like hydrolase	3.4e-21	83.8	1	28-282
1820	Fe_hyd_1 g_C	Iron only hydrogenase large subunit, C- te	1.3e-92	321.1	1	204-516
1820	Fe_hyd_S SU	Iron hydrogenase small subunit	8.3	-13.1	1	529-576
1821	filament	Intermediate filament protein	1e-143	490.8	1	55-366
1822	Keratin_B 2	Keratin, high sulfur B2 protein	0.082	-51.3	1	12-174
1824	metalthio	Metallothionein	5.7e-17	69.8	1	48-108
1824	AFP	Insect antifreeze protein	2.6	14.5	1	61-72
1825	C2	C2 domain	4.7e-53	189.7	2	373- 462:528- 617
1825	RPH3A_e ffector	Rabphilin-3A effector domain	0.035	-127.1	1	1-237
1825	zf-MIZ	MIZ zinc finger	0.4	-10.5	1	80-111
1825	PHD	PHD-finger	0.97	-9.7	1	62-108
1825	LIM	LIM domain	2.2	-14.6	1	80-128
1825	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	3.1	-4.0	1	63-105
1828	efhand	EF hand	8.4e-08	39.4	3	106- 134:142- 170:407- 435
1829	60s_ribos omal	60s Acidic ribosomal protein	7.4	-38.2	1	163-291
1831	Tektin	Tektin family	1.6	-227.3	1	1-150
1833	EGF	EGF-like domain	1.1e-32	122.0	5	26-54:57- 85:92- 124:156- 187:194- 226
1833	laminin_E GF	Laminin EGF-like (Domains III and V)	1.6	-5.9	1	29-63
1833	Bowman- Birk_leg	Bowman-Birk serine protease inhibitor	4.8	-16.7	1	37-85
1833	metalthio	Metallothionein	5.5	-10.1	1	59-117
1834	7tm_1	7 transmembrane receptor (rhodopsin family)	4.8e-05	-0.8	1	31-273
1834	7tm_2	7 transmembrane receptor (Secretin family)	5.5	-151.6	1	9-248
1835	rrm	RNA recognition motif.	0.05	15.7	1	75-141
1835	Met_10	Met-10+ like-protein	0.065	-100.4	1	333-583
1835	UPF0020	Putative RNA methylase family UPF0020	0.073	-53.8	1	410-566
1835	PCMT	Protein-L-isoaspartate(D-aspartate) O-	0.2	-114.1	1	391-543
1835	Methyltra nsf_4	Putative methyltransferase	2.1	-82.0	1	424-566
1835	notch	Notch (DSL) domain	6.1	-10.5	1	233-271
1836	Kelch	Kelch motif	3e-33	123.9	4	242- 288:290- 331:333- 378:380- 435
1836	BTB	BTB/POZ domain	2.3	-15.2	1	1-129
1837	tsp_1	Thrombospondin type 1 domain	0.0014	23.3	5	139- 196:203- 256:257-

SEQ ID	Model	Description	E-value	Score	Repeats	Position
						313:320-370:374-432
1837	EB	EB module	6.4	-10.5	1	330-399
1838	adh_zinc	Zinc-binding dehydrogenase	7.3e-55	195.7	1	44-369
1838	Lipase_GDSL	Lipase/Acylhydrolase with GDLS-like motif	5.5	-20.4	1	103-189
1839	pkinase	Protein kinase domain	2.4e-05	-58.0	1	81-333
1841	zf-C2H2	Zinc finger, C2H2 type	4.4e-30	113.4	7	141-163:169-191:197-219:225-247:350-372:378-400:406-434
1841	KRAB	KRAB box	5.1e-23	89.9	1	44-84
1841	TFIIS	Transcription factor S-II (TFIIS)	2.4	-1.9	1	144-179
1841	Lentiviral_Tat	Lentiviral Tat protein	4.9	-23.0	1	35-125
1841	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	7.2	-7.1	1	352-411
1841	rubredoxin	Rubredoxin	7.4	-11.1	1	403-433
1842	E2F_TDP	Transcription factor E2F/dimerisation partne	1.5	-95.1	1	18-229
1843	V_ATPase_sub_a	V-type ATPase 116kDa subunit family	0	1258.7	1	26-831
1843	UCR_14kD	Ubiquinol-cytochrome C reductase compl	3.2	-40.4	1	6-112
1843	FlpP	FlpP family	4.8	-148.9	1	533-661
1843	PsbH	Photosystem II 10 kDa phosphoprotein	7.1	5.1	1	751-803
1844	aa_permeases	Amino acid permease	5.6e-08	-125.3	1	28-529
1844	Aa_transpro	Transmembrane amino acid transporter pro	0.71	-178.9	1	30-408
1844	BPD_transp_2	Branched-chain amino acid transport syst	3.3	-116.9	1	175-440
1844	MVIN	Virulence factor MVIN	3.5	-240.9	1	87-515
1844	FecCD	FecCD transport family	5.3	-216.0	1	311-521
1844	ion_trans	Ion transport protein	6.2	-11.7	1	288-495
1844	7tm_5	7TM chemoreceptor	7.1	-168.6	1	238-498
1848	sugar_tr	Sugar (and other) transporter	0.0072	-107.9	1	12-407
1848	xan_ur_permease	Permease family	5.6	-196.7	1	38-359
1848	FecCD	FecCD transport family	6.3	-217.4	1	56-287
1848	Nucleoside_trans	Nucleoside transporter	8.1	-162.4	1	82-365
1848	Pucc	Pucc protein	9.8	-283.2	1	51-403
1849	Filamin	Filamin/ABP280 repeat	2.3e-20	81.1	1	396-494
1849	zf-B_box	B-box zinc finger	9.3e-11	49.2	2	130-176:186-227
1849	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.0016	24.4	1	29-62
1853	ank	Ankyrin repeat	1.1e-98	341.3	10	485-517:518-550:551-583:584-616:617-

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						650:651- 683:684- 716:717- 749:750- 780:782- 814
1853	pkinase	Protein kinase domain	1.6e-50	181.3	1	22-286
1854	ras	Ras family	1.4e-13	17.8	1	5-194
1855	Acyltransf erase	Acyltransferase	3e-34	127.2	1	92-289
1856	wap	WAP-type (Whey Acidic Protein) 'four-disulfi	0.0025	18.7	1	31-72
1857	arf	ADP-ribosylation factor family	2.5e-11	24.6	1	7-193
1857	GTP_EFT U	Elongation factor Tu GTP binding domain	1.6	-82.5	1	19-198
1858	zf-C2H2	Zinc finger, C2H2 type	2.1e-09	44.7	5	82- 104:110- 132:138- 161:364- 386:392- 416
1858	PHD	PHD-finger	7.7	-18.1	1	365-400
1859	zf-C2H2	Zinc finger, C2H2 type	7.2e-20	79.4	4	119- 141:147- 169:175- 198:214- 237
1860	BTB	BTB/POZ domain	1.7e-29	111.4	1	22-126
1860	zf-C2H2	Zinc finger, C2H2 type	5.1e-14	60.0	3	373- 395:401- 423:429- 452
1860	K_tetra	K+ channel tetramerisation domain	0.44	-30.2	1	34-124
1860	zf-BED	BED zinc finger	8.9	-6.9	1	363-396
1861	SNF2_N	SNF2 and others N-terminal domain	2.1e-72	254.0	1	137-473
1861	helicase_ C	Helicase conserved C-terminal domain	1.4e-24	95.1	1	559-632
1861	DEAD	DEAD/DEAH box helicase	0.26	-59.6	1	124-337
1861	SEC-C	SEC-C motif	0.43	13.8	1	426-446
1862	ras	Ras family	2.4e-69	243.8	1	19-217
1862	arf	ADP-ribosylation factor family	4.1e-05	-53.5	1	1-182
1864	rrm	RNA recognition motif.	0.053	15.4	1	129-191
1867	T-box	T-box	4.3e-09	29.9	1	1-92
1870	F-box	F-box domain	1.8	15.0	1	124-171
1871	PH	PH domain	1.1e-13	58.9	1	170-273
1872	isodh	Isocitrate/isopropylmalate dehydrogenase	1.4e- 123	423.9	1	10-383
1873	ank	Ankyrin repeat	1.8e-08	41.5	2	39-71:72- 104
1874	ank	Ankyrin repeat	1.8e-08	41.5	2	67-99:100- 132
1875	PAP2	PAP2 superfamily	0.0034	13.0	1	1-107
1876	DUF51	Protein of unknown function DUF51	5.7e-13	52.5	1	107-261
1877	zf-C2H2	Zinc finger, C2H2 type	1.5e-72	254.5	9	285- 307:313- 335:341- 363:369- 391:397-

SEQ ID	Model	Description	E-value	Score	Repeats	Position
						419:425- 447:451- 473:479- 501:507- 529
1877	KRAB	KRAB box	2.7e-21	84.2	1	49-89
1877	zf-BED	BED zinc finger	0.74	2.7	1	344-392
1877	TFIIS	Transcription factor S-II (TFIIS)	1.5	-0.0	1	369-407
1877	GATA	GATA zinc finger	2.1	-7.1	1	477-524
1877	LIM	LIM domain	2.5	-15.1	1	371-435
1877	E6	Early Protein (E6)	5.7	-66.7	1	315-402
1878	AAA	ATPase family associated with various	1.3e-62	221.4	1	217-409
1878	Sigma54_ activat	Sigma-54 interaction domain	4.6	-165.4	1	184-365
1879	SSF	Sodium:solute symporter family	4.8e- 170	578.3	1	58-460
1880	SSF	Sodium:solute symporter family	1.3e- 198	673.2	1	58-487
1881	perilipin	Perilipin family	6.7e-53	189.2	1	12-369
1882	aminotran 1_2	Aminotransferase class I and II	7.5e-07	25.0	1	165-515
1883	DSPc	Dual specificity phosphatase, catalytic doma	2.5e-30	114.2	1	54-199
1884	ig	Immunoglobulin domain	7.2e-14	59.5	2	34- 111:155- 229
1885	MCM	MCM2/3/5 family	4.6e-12	-67.3	1	106-391
1886	Kelch	Kelch motif	1.8e-63	224.3	6	262- 306:309- 356:358- 403:405- 453:455- 495:497- 544
1886	BTB	BTB/POZ domain	5.3e-32	119.7	1	26-134
1887	UBA	UBA/TS-N domain	1.9e-05	31.5	1	726-765
1887	rrm	RNA recognition motif.	0.00026	27.8	1	1342-1407
1887	MARCKS	MARCKS family	4.3	-90.8	1	270-571
1888	UBA	UBA/TS-N domain	1.9e-05	31.5	1	726-765
1888	rrm	RNA recognition motif.	0.00026	27.8	1	1303-1368
1888	MARCKS	MARCKS family	4.3	-90.8	1	270-571
1889	UBA	UBA/TS-N domain	1.9e-05	31.5	1	726-765
1889	rrm	RNA recognition motif.	0.00026	27.8	1	1245-1310
1889	MARCKS	MARCKS family	4.3	-90.8	1	270-571
1889	Atrophin- 1	Atrophin-1 family	6.9	-676.1	1	237-986
1890	Na_H_Ex changer	Sodium/hydrogen exchanger family	2.4e-18	74.4	1	119-520
1890	Na_Ca_E x	Sodium/calcium exchanger protein	3.1	-43.6	1	270-384
1890	7tm_5	7TM chemoreceptor	3.8	-163.7	1	259-503
1890	Abi	CAAX amino terminal protease family	5.9	-25.8	1	309-401
1890	oxidored_ ql	NADH-Ubiquinone/plastoquinone	7.9	-169.7	1	251-502
1891	Acyl- CoA_hydr o	Cytosolic long-chain acyl-CoA thioeste	8.9e-72	251.9	2	26- 168:200- 336
1891	tRNA_ant	OB-fold nucleic acid binding domain	3.5	5.8	1	230-307

SEQ ID	Model	Description	E-value	Score	Repeats	Position
	i					
1892	zf-DHHC	DHHC zinc finger domain	8.6e-18	72.5	1	145-207
1894	SPRY	SPRY domain	4.5e-11	50.2	1	353-474
1894	fn3	Fibronectin type III domain	0.054	17.6	1	165-258
1895	dsrcm	Double-stranded RNA binding motif	1.5e-12	55.1	2	229-293:337-401
1895	WW	WW domain	0.00016	28.5	1	20-49
1896	SPRY	SPRY domain	9.9e-26	98.9	1	186-301

TABLE 5

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
951	1e07	A	279	369	5.7e-21	0.77	1.00		EPIDERMAL GROWTH FACTOR RECEPTOR PATHWAY CHAIN: A;	SIGNALING PROTEIN CALCIUM BINDING, SIGNALING DOMAIN, NPF BINDING, FW BINDING, 2 EF-HAND, EH DOMAIN, SIGNALING PROTEIN
951	1e07	A	4	98	1.7e-07	-0.14	0.88		EPIDERMAL GROWTH FACTOR RECEPTOR PATHWAY CHAIN: A;	SIGNALING PROTEIN CALCIUM BINDING, SIGNALING DOMAIN, NPF BINDING, FW BINDING, 2 EF-HAND, EH DOMAIN, SIGNALING PROTEIN
951	1ell		293	345	3.8e-05	-0.02	0.22		CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) 1CLL 3	
951	1eh2		278	369	1.1e-31	0.58	1.00		EPS15; CHAIN: NULL;	CALCIUM BINDING EH2, EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE CALCIUM BINDING, SIGNALING DOMAIN, NPF BINDING, EF-HAND, EH 2 DOMAIN
951	1eh2		3	97	6.8e-11	0.72	0.99		EPS15; CHAIN: NULL;	CALCIUM BINDING EH2, EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE CALCIUM BINDING, SIGNALING DOMAIN, NPF BINDING, EF-HAND, EH 2 DOMAIN
951	1irro		280	348	1.3e-05	0.33	0.98		CALCIUM-BINDING PROTEIN RAT ONCOMODULIN 1RRO 3	
951	1trc	A	284	345	1.5e-05	-0.21	0.23		CALCIUM BINDING PROTEIN CALMODULIN (/TR=2=CS\$ FRAGMENT COMPRISING RESIDUES 78 - 148 1TRC 3 OF THE INTACT MOLECULE) 1TRC 4	
951	1vrk	A	293	345	3.8e-05	-0.39	0.15		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
951	2pvh	A	293	348	3.8e-05	-0.13	0.25		PARVALBUMIN; CHAIN: A;	METAL BINDING PROTEIN CALCIUM BINDING PROTEIN
951	2scp	A	283	345	5.7e-06	-0.13	0.47		BINDING PROTEIN SARCOPLASMIC CALCIUM-BINDING PROTEIN 2SCP 3	
952	1a75	A	310	389	0.00095	-0.81	0.05		PARVALBUMIN; CHAIN: A, B	CALCIUM BINDING PROTEIN CALCIUM BINDING PROTEIN, MUSCLE PROTEIN
952	1aj4		280	377	5.7e-05	0.02	0.17		TROPONIN C; CHAIN: NULL;	MUSCLE PROTEIN CTNC; CARDIAC, MUSCLE PROTEIN, REGULATORY, CALCIUM BINDING
952	1aui	B	280	377	0.00038	-0.03	0.13		SERINE/THREONINE PHOSPHATASE 2B; CHAIN: A, B;	HYDROLASE CALCINEURIN; HYDROLASE, PHOSPHATASE, IMMUNOSUPPRESSION
952	1br1	B	282	377	0.0019	-0.05	0.18		MYOSIN; CHAIN: A, B, C, D, E, F, G, H;	MUSCLE PROTEIN MDE; MUSCLE PROTEIN
952	1bu3		310	389	0.0038	-0.24	0.05		CALCIUM-BINDING PROTEIN; CHAIN: NULL;	CALCIUM BINDING CALCIUM BINDING
952	1c07	A	279	369	5.7e-21	0.77	1.00		EPIDERMAL GROWTH FACTOR RECEPTOR PATHWAY CHAIN: A;	SIGNALING PROTEIN CALCIUM BINDING; SIGNALING DOMAIN, NPF BINDING; FW BINDING, 2 EF-HAND, EH DOMAIN, SIGNALING PROTEIN
952	1c07	A	4	99	5.1e-12	0.10	0.90		EPIDERMAL GROWTH FACTOR RECEPTOR PATHWAY CHAIN: A;	SIGNALING PROTEIN CALCIUM BINDING; SIGNALING DOMAIN, NPF BINDING; FW BINDING, 2 EF-HAND, EH DOMAIN, SIGNALING PROTEIN
952	1cll		293	345	3.8e-05	-0.02	0.22		CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) 1CLL 3	
952	1dfl	A	280	389	0.0038	-0.16	0.18		CARDIAC TROPONIN C; CHAIN: A;	STRUCTURAL PROTEIN HELIX- TURN-HELIX
952	1eh2		278	369	1.1e-31	0.58	1.00		EPS15; CHAIN: NULL;	CALCIUM BINDING EH2, EPIDERMAL GROWTH FACTOR

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
952	1eh2		3	97	1.7e-13	0.81	0.99		EPS15; CHAIN: NULL;	RECEPTOR SUBSTRATE CALCIUM BINDING, SIGNALING DOMAIN, NPF BINDING, EF-HAND, EH 2 DOMAIN
952	1qjt	A	14	97	1.7e-08	0.64	0.80		EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE CALCIUM BINDING, SIGNALING DOMAIN, NPF BINDING, EF-HAND, EH 2 DOMAIN	EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE CALCIUM BINDING, SIGNALING DOMAIN, NPF BINDING, EF-HAND, EH 2 DOMAIN
952	1rro		280	348	1.3e-05	0.33	0.98		CALCIUM-BINDING PROTEIN RAT ONCOMODULIN 1RRO 3	GROWTH FACTOR EHI; EH DOMAIN, EPS15, EF-HAND, SOLUTION STRUCTURE, S100 PROTEIN
952	1trc	A	284	345	1.5e-05	-0.21	0.23		CALCIUM BINDING PROTEIN CALMODULIN (TR=2=C\$ FRAGMENT COMPRISING RESIDUES 78 - 148 1TRC 3 OF THE INTACT MOLECULE) 1TRC 4	
952	1vrk	A	280	377	0.00038	-0.23	0.49		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
952	1vrk	A	293	345	3.8e-05	-0.39	0.15		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
952	2pvb	A	293	348	3.8e-05	-0.13	0.25		PARVALBUMIN; CHAIN: A;	METAL BINDING PROTEIN
952	2scp	A	283	345	5.7e-06	-0.13	0.47		BINDING PROTEIN SARCOPLASMIC CALCIUM-BINDING PROTEIN 2SCP 3	CALCIUM BINDING PROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
953	1a09	A	319	413	3.8e-17	0.34	0.98		C-SRC TYROSINE KINASE; CHAIN: A, B; ACE-FORMYL PHOSPHOTYR-GLU-(N,N-DIPENTYL AMINE); CHAIN: C, D;	COMPLEX (TRANSFERASE/PEPTIDE) COMPLEX (TRANSFERASE/PEPTIDE)
953	1a81	A	255	413	1.5e-18	0.27	0.72		SYK KINASE; CHAIN: A, C, E, G, I, K; T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN; CHAIN: B, D, F, H, J, L;	COMPLEX (TRANSFERASE/PEPTIDE) ITAM PEPTIDE; COMPLEX (TRANSFERASE/PEPTIDE) SYK, KINASE, SH2 DOMAIN, ITAM
953	1ab2		319	417	3.8e-17	0.02	0.63		TRANSFERASE(PHOSPHOTRANSFERASE) PROTO-ONCOGENE TYROSINE KINASE (E.C.2.7.1.112) 1AB2 3 (SRC HOMOLOG 2 DOMAIN) (ABELSON, SH2 ABL) 1AB2 4 (NMR, 20 STRUCTURES) 1AB2 5	
953	1aot	F	319	413	1.7e-17	0.46	0.99		FYN PROTEIN-TYROSINE KINASE; CHAIN: F; PHOSPHOTYROSYL PEPTIDE; CHAIN: P	COMPLEX (PROTO-ONCOGENE/EARLY PROTEIN) SRC HOMOLOG 2 DOMAIN; SH2 DOMAIN, SIGNAL TRANSDUCTION, PEPTIDE COMPLEX, 2 COMPLEX (PROTO-ONCOGENE/EARLY PROTEIN)
953	1aya	A	317	412	7.6e-18	0.18	1.00		HYDROLASE(SH2 DOMAIN) TYROSINE PHOSPHATASE SYP (N-TERMINAL SH2 DOMAIN) 1AYA 3 (PTPID, SHPTP2) (E.C.3.1.3.48) COMPLEXED WITH THE PEPTIDE 1AYA 4 PDGFR-1009 1AYA 5	
953	1bfi		319	418	3.8e-19	0.36	0.82		P85 ALPHA; CHAIN: NULL;	SH2 DOMAIN PHOSPHATIDYLINOSITOL 3-KINASE REGULATORY ALPHA SH2

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
953	1csy	A	319	416	3.8e-19	0.33	0.82		SYK PROTEIN TYROSINE KINASE; CHAIN: A; ACETYL-THR-PTR-GLU-THR-LEU-NH2; CHAIN: B;	DOMAIN, P85ALPHA, PI 3-KINASE, NMR, C TERMINAL SH2 2 DOMAIN COMPLEX (PHOSPHOTRANSFERASE/PEPTIDE) PROTEIN-TYROSINE KINASE SH2 DOMAIN, COMPLEX 2 (PHOSPHOTRANSFERASE/PEPTIDE)
953	1cun	A	140	228	0.00013	0.05	0.06		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
953	1dlz	B	320	413	5.7e-18	0.04	0.49		SAP SH2 DOMAIN; CHAIN: A, B, C, D;	GENE REGULATION SH2 DOMAINS
953	1d4t	A	319	413	1.9e-19	0.22	0.75		T CELL SIGNAL TRANSDUCTION MOLECULE SAP; CHAIN: A; SIGNALING LYMPHOCYTIC ACTIVATION MOLECULE; CHAIN: B;	SIGNALING PROTEIN SLAM; SH2 DOMAIN, TYROSINE KINASE, SIGNAL TRANSDUCTION, PEPTIDE 2 RECOGNITION
953	1fhs		312	425	0.0017			58.62	GROWTH FACTOR RECEPTOR BOUND PROTEIN-2; CHAIN: NULL;	SH2 DOMAIN GRB2; GRB2, SH2 DOMAIN, PROTEIN NMR, SOLUTION STRUCTURES
953	2pld	A	319	417	9.5e-19	0.32	0.49		PHOSPHORIC DIESTER HYDROLASE PHOSPHOLIPASE C-GAMMA-1 (E.C.3.1.4.11) (C-TERMINAL SH2 2PLD 3 DOMAIN COMPRISING RESIDUES 663 - 759) COMPLEXED WITH A 2PLD 4 PHOSPHOPEPTIDE FROM THE PLATELET-DERIVED GROWTH FACTOR 2PLD 5 RECEPTOR (RESIDUES 1018 - 1029; ASP-ASN-ASP-PTYR-ILE-ILE- 2PLD 6	

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									PRO-LEU-PRO-ASP-PRO-LYS) (NMR, MINIMIZED AVERAGE STRUCTURE) 2PLD 7	
954	1a09	A	346	440	3.8e-17	0.34	0.98		C-SRC TYROSINE KINASE; CHAIN: A, B; ACE-FORMYL PHOSPHOTYR-GLU-(N,N- DIPENTYL AMINE); CHAIN: C, D;	COMPLEX (TRANSFERASE/PEPTIDE) COMPLEX (TRANSFERASE/PEPTIDE)
954	1a81	A	282	440	1.5e-18	0.27	0.72		SYK KINASE; CHAIN: A, C, E, G, I, K; T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN; CHAIN: B, D, F, H, J, L;	COMPLEX (TRANSFERASE/PEPTIDE) ITAM PEPTIDE; COMPLEX (TRANSFERASE/PEPTIDE), SYK, KINASE, SH2 DOMAIN, ITAM
954	1ab2		346	444	3.8e-17	0.02	0.63		TRANSFERASE(PHOSPHOTRA NSFERASE) PROTO- ONCOGENE TYROSINE KINASE (E.C.2.7.1.112) 1AB2 3 (SRC HOMOLOG Y 2 DOMAIN) (ABELSON, SH2 ABL) 1AB2 4 (NMR, 20 STRUCTURES) 1AB2 5	
954	1aot	F	346	440	1.7e-17	0.46	0.99		FYN PROTEIN-TYROSINE KINASE; CHAIN: F; PHOSPHOTYROSYL PEPTIDE; CHAIN: P	COMPLEX (PROTO- ONCOGENE/EARLY PROTEIN) SRC HOMOLOGY 2 DOMAIN; SH2 DOMAIN, SIGNAL TRANSDUCTION, PEPTIDE COMPLEX, 2 COMPLEX (PROTO-ONCOGENE/EARLY PROTEIN)
954	1aya	A	344	439	7.6e-18	0.18	1.00		HYDROLASE(SH2 DOMAIN) TYROSINE PHOSPHATASE SYP (N-TERMINAL SH2 DOMAIN) 1AYA 3 (PTP1D, SHPTP2) (E.C.3.1.3.48) COMPLEXED WITH THE PEPTIDE 1AYA 4	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
954	1bfi		346	445	3.8e-19	0.36	0.82		PDGFR-1009 1A YA 5 P85 ALPHA; CHAIN: NULL;	SH2 DOMAIN PHOSPHATIDYLINOSITOL 3-KINASE REGULATORY ALPHA SH2 DOMAIN, P85ALPHA, PI 3-KINASE, NMR, C TERMINAL SH2 2 DOMAIN
954	1csy	A	346	443	3.8e-19	0.33	0.82		SYK PROTEIN TYROSINE KINASE; CHAIN: A; ACETYL- THR-PTR-GLU-THR-LEU-NH2; CHAIN: B;	COMPLEX (PHOSPHOTRANSFERASE/PEPTIDE) PROTEIN-TYROSINE KINASE SH2 DOMAIN, COMPLEX 2 (PHOSPHOTRANSFERASE/PEPTIDE)
954	1dlz	B	347	440	5.7e-18	0.04	0.49		SAP SH2 DOMAIN; CHAIN: A, B, C, D;	GENE REGULATION SH2 DOMAINS
954	1d4t	A	346	440	1.9e-19	0.22	0.75		T CELL SIGNAL TRANSDUCTION MOLECULE SAP; CHAIN: A; SIGNALING LYMPHOCYTIC ACTIVATION MOLECULE; CHAIN: B;	SIGNALING PROTEIN SLAM; SH2 DOMAIN, TYROSINE KINASE, SIGNAL TRANSDUCTION, PEPTIDE 2 RECOGNITION
954	2pld	A	346	444	9.5e-19	0.32	0.49		PHOSPHORIC DIESTER HYDROLASE PHOSPHOLIPASE C-GAMMA-1 (E.C.3.1.4.11) (C- TERMINAL SH2 2PLD 3 DOMAIN COMPRISING RESIDUES 663 - 759) COMPLEXED WITH A 2PLD 4 PHOSPHOPEPTIDE FROM THE PLATELET-DERIVED GROWTH FACTOR 2PLD 5 RECEPTOR (RESIDUES 1018 - 1029: ASP- ASN-ASP-PTYR-ILE-ILE- 2PLD 6 PRO-LEU-PRO-ASP-PRO-LYS) (NMR, MINIMIZED AVERAGE STRUCTURE) 2PLD 7	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
955	1a12	A	35	427	1.7e-77			150.38	REGULATOR OF CHROMOSOME CONDENSATION 1; CHAIN: A, B, C;	GUANINE NUCLEOTIDE EXCHANGE FACTOR RCC1; GUANINE NUCLEOTIDE EXCHANGE FACTOR, GEF, RAN, 2 RAS-LIKE NUCLEAR GTP BINDING PROTEIN HEADER TER
955	1a12	A	51	423	1.7e-77	0.69	1.00		REGULATOR OF CHROMOSOME CONDENSATION 1; CHAIN: A, B, C;	GUANINE NUCLEOTIDE EXCHANGE FACTOR RCC1; GUANINE NUCLEOTIDE EXCHANGE FACTOR, GEF, RAN, 2 RAS-LIKE NUCLEAR GTP BINDING PROTEIN HEADER TER
957	1azw	A	85	183	0.0076	-0.16	0.05		PROLINE IMINOPEPTIDASE; CHAIN: A, B;	AMINOPEPTIDASE AMINOPEPTIDASE, PROLINE IMINOPEPTIDASE, SERINE PROTEASE, 2 XANTHOMONAS CAMPESTRIS
957	1cvl		166	204	0.00038	-0.67	0.49		TRIACYLGLYCEROL HYDROLASE; CHAIN: NULL;	HYDROLASE TRIACYLGLYCEROL-HYDROLASE, X-RAY CRYSTALLOGRAPHY, 2 PSEUDOMONADACEAE, OXYANION, CIS-PEPTIDE, HYDROLASE
957	1ei9	A	86	204	7.6e-05	0.14	0.57		PALMITOYL PROTEIN THIOESTERASE 1; CHAIN: A;	HYDROLASE ALPHA/BETA HYDROLASE, GLYCOPROTEIN
957	4lip	D	165	204	0.0048	-0.60	0.23		TRIACYLGLYCEROL-HYDROLASE; CHAIN: D, E;	LIPASE LIPASE; LIPASE, HYDROLASE, PSEUDOMONADACEAE, COVALENT INTERMEDIATE, 2 TRIGLYCERIDE ANALOGUE, ENANTIOSELECTIVITY
962	1ayz	A	2	121	3.8e-38	0.57	1.00		UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN CONJUGATION UBC2; UBIQUITIN CONJUGATION,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										UBIQUITIN-CONJUGATING ENZYME
962	1ayz	A	2	121	3.8e-38			124.83	UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN CONJUGATION UBC2; UBIQUITIN CONJUGATION, UBIQUITIN-CONJUGATING ENZYME
962	1ayz	A	2	121	5.1e-37	0.63	1.00		UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN CONJUGATION UBC2; UBIQUITIN CONJUGATION, UBIQUITIN-CONJUGATING ENZYME
962	1qcq	A	1	119	3.4e-40	0.62	1.00		UBIQUITIN CONJUGATING ENZYME; CHAIN: A;	LIGASE UBIQUITIN, UBIQUITIN-CONJUGATING ENZYME, YEAST
962	1qcq	A	3	120	3.4e-40			70.02	UBIQUITIN CONJUGATING ENZYME; CHAIN: A;	LIGASE UBIQUITIN, UBIQUITIN-CONJUGATING ENZYME, YEAST
962	2aak		1	119	3.4e-37	0.59	1.00		UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION UBC1; UBIQUITIN CONJUGATION, LIGASE
962	2aak		1	120	3.4e-37			141.95	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION UBC1; UBIQUITIN CONJUGATION, LIGASE
963	1ayz	A	2	136	1.5e-46	1.15	1.00		UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN CONJUGATION UBC2; UBIQUITIN CONJUGATION, UBIQUITIN-CONJUGATING ENZYME
963	1ayz	A	2	136	1.9e-48	0.91	1.00		UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN CONJUGATION UBC2; UBIQUITIN CONJUGATION, UBIQUITIN-CONJUGATING ENZYME
963	1ayz	A	2	136	1.9e-48			162.79	UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN CONJUGATION UBC2; UBIQUITIN CONJUGATION, UBIQUITIN-CONJUGATING ENZYME
963	1qcq	A	1	134	1.5e-50	0.63	1.00		UBIQUITIN CONJUGATING ENZYME; CHAIN: A;	LIGASE UBIQUITIN, UBIQUITIN-CONJUGATING ENZYME, YEAST
963	1qcq	A	3	135	1.5e-50			102.58	UBIQUITIN CONJUGATING	LIGASE UBIQUITIN, UBIQUITIN-

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
963	2aak		1	134	3.4e-48	0.88	1.00		ENZYME; CHAIN: A;	CONJUGATING ENZYME, YEAST
963	2aak		1	135	3.4e-48			179.88	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL; UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION UBC1; UBIQUITIN CONJUGATION, LIGASE UBIQUITIN CONJUGATION UBC1; UBIQUITIN CONJUGATION, LIGASE
971	1bg2		6	371	0			207.35	KINESIN; CHAIN: NULL;	MOTOR PROTEIN MOTOR PROTEIN, ATPASE, MICROTUBULE ASSOCIATED
971	1bg2		7	371	0	0.39	1.00		KINESIN; CHAIN: NULL;	MOTOR PROTEIN MOTOR PROTEIN, ATPASE, MICROTUBULE ASSOCIATED
971	1cz7	A	5	372	1.7e-81	0.33	1.00		MICROTUBULE MOTOR PROTEIN NCD; CHAIN: A, B, C, D;	CONTRACTILE PROTEIN NCD, CLARET SEGREGATIONAL PROTEIN; NCD CRYSTAL STRUCTURE, MICROTUBULE MOTORS, KINESIN 2 SUPERFAMILY, CONTRACTILE PROTEIN
971	1cz7	A	7	372	1.7e-98			139.50	MICROTUBULE MOTOR PROTEIN NCD; CHAIN: A, B, C, D;	CONTRACTILE PROTEIN NCD, CLARET SEGREGATIONAL PROTEIN; NCD CRYSTAL STRUCTURE, MICROTUBULE MOTORS, KINESIN 2 SUPERFAMILY, CONTRACTILE PROTEIN
971	1cz7	A	9	372	1.7e-98	0.34	1.00		MICROTUBULE MOTOR PROTEIN NCD; CHAIN: A, B, C, D;	CONTRACTILE PROTEIN NCD, CLARET SEGREGATIONAL PROTEIN; NCD CRYSTAL STRUCTURE, MICROTUBULE MOTORS, KINESIN 2 SUPERFAMILY, CONTRACTILE PROTEIN
971	1dn1	B	647	825	1.3e-15	0.15	-0.18		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
971	1erj	A	1269	1643	1.7e-78	0.54	0.98		TRANSCRIPTIONAL	TRANSCRIPTION INHIBITOR BETA-

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									REPRESSOR TUPI; CHAIN: A, B, C;	PROPELLER
971	1got	B	1229	1600	1e-98			115.67	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
971	1got	B	1317	1640	1e-98	0.88	1.00		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
971	1got	B	1429	1660	3.4e-46	0.42	1.00		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
971	2kin	A	3	260	1.5e-71			135.00	KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
971	2kin	A	7	281	1.5e-71	0.09	1.00		KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
971	2kin	B	296	380	1.7e-36	-0.48	0.99		KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
971	2ncd	A	5	370	1e-81	0.34	1.00		KINESIN MOTOR NCD; CHAIN: A;	CONTRACTILE PROTEIN KINESIN, MICROTUBULE-BASED MOTOR,

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
971	2ncd	A	7	371	1e-81			132.55	KINESIN MOTOR NCD; CHAIN: A;	NCD, CONTRACTILE PROTEIN CONTRACTILE PROTEIN KINESIN, MICROTUBULE-BASED MOTOR, NCD, CONTRACTILE PROTEIN
971	3kar		8	370	1.9e-91			165.99	KINESIN-LIKE PROTEIN KAR3; CHAIN: NULL;	CONTRACTILE PROTEIN CONTRACTILE PROTEIN, KAR3, KINESIN-RELATED PROTEIN, MOTOR 2 PROTEIN, ATPASE, P-LOOP, MICROTUBULE BINDING PROTEIN
971	3kar		8	370	1e-83	0.30	1.00		KINESIN-LIKE PROTEIN KAR3; CHAIN: NULL;	CONTRACTILE PROTEIN CONTRACTILE PROTEIN, KAR3, KINESIN-RELATED PROTEIN, MOTOR 2 PROTEIN, ATPASE, P-LOOP, MICROTUBULE BINDING PROTEIN
971	3kar		9	370	1.9e-91	0.19	1.00		KINESIN-LIKE PROTEIN KAR3; CHAIN: NULL;	CONTRACTILE PROTEIN CONTRACTILE PROTEIN, KAR3, KINESIN-RELATED PROTEIN, MOTOR 2 PROTEIN, ATPASE, P-LOOP, MICROTUBULE BINDING PROTEIN
971	3kin	B	298	380	3.8e-35	-0.23	1.00		KINESIN HEAVY CHAIN; CHAIN: A, B, C, D;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
971	3kin	B	298	405	6.8e-28	-0.39	1.00		KINESIN HEAVY CHAIN; CHAIN: A, B, C, D;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
975	1buo	A	5	125	1.7e-20	0.20	1.00		PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;	GENE REGULATION POZ DOMAIN; PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2 REPRESSOR, ZINC-FINGER PROTEIN, X-RAY CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
975	1buo	A	5	128	3.8e-28	0.41	0.99		PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;	LEUKEMIA, GENE REGULATION
975	1buo	A	5	130	3.8e-28			58.76	PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;	GENE REGULATION POZ DOMAIN; PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2 REPRESSOR, ZINC-FINGER PROTEIN, X-RAY CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC LEUKEMIA, GENE REGULATION
975	1gof		251	464	0.0022	0.10	0.19		OXIDOREDUCTASE(OXYGEN(A)) GALACTOSE OXIDASE (E.C.1.1.3.9) (PH 4.5) 1GOF 3	GENE REGULATION POZ DOMAIN; PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2 REPRESSOR, ZINC-FINGER PROTEIN, X-RAY CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC LEUKEMIA, GENE REGULATION
975	1gof		288	385	5.1e-10	0.03	-0.02		OXIDOREDUCTASE(OXYGEN(A)) GALACTOSE OXIDASE (E.C.1.1.3.9) (PH 4.5) 1GOF 3	
977	1bg2		1	352	6.8e-81			220.57	KINESIN; CHAIN: NULL;	MOTOR PROTEIN MOTOR PROTEIN, ATPASE, MICROTUBULE ASSOCIATED
977	1bg2		2	352	6.8e-81	0.74	1.00		KINESIN; CHAIN: NULL;	MOTOR PROTEIN MOTOR PROTEIN, ATPASE, MICROTUBULE ASSOCIATED
977	1cz7	A	3	352	8.5e-69			160.51	MICROTUBULE MOTOR PROTEIN NCD; CHAIN: A, B, C, D;	CONTRACTILE PROTEIN NCD, CLARET SEGREGATIONAL PROTEIN; NCD CRYSTAL STRUCTURE, MICROTUBULE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
977	1cz7	A	5	354	8.5e-69	0.58	1.00		MICROTUBULE MOTOR PROTEIN NCD; CHAIN: A, B, C, D;	MOTORS, KINESIN 2 SUPERFAMILY, CONTRACTILE PROTEIN
977	1dn1	B	365	430	5.7e-05	0.21	0.16		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
977	1fio	A	582	766	0.0057	-0.00	0.10		SSO1 PROTEIN; CHAIN: A;	MEMBRANE PROTEIN FOUR HELIX BUNDLE, ALPHA HELIX
977	2kin	A	1	259	5.2e-72			151.15	KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
977	2kin	A	1	259	5.7e-72			151.15	KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
977	2kin	A	2	258	1.2e-55	0.38	1.00		KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
977	2kin	A	2	259	5.7e-72	0.45	1.00		KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
977	2kin	B	272	366	1.7e-17	-0.24	1.00		KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
977	2kin	B	274	364	1.9e-36	-0.22	1.00		KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
977	2ncd	A	3	352	1.2e-68			157.70	KINESIN MOTOR NCD; CHAIN: A;	CONTRACTILE PROTEIN KINESIN, MICROTUBULE-BASED MOTOR, NCD, CONTRACTILE PROTEIN
977	2ncd	A	5	346	1.2e-68	0.64	1.00		KINESIN MOTOR NCD; CHAIN: A;	CONTRACTILE PROTEIN KINESIN, MICROTUBULE-BASED MOTOR, NCD, CONTRACTILE PROTEIN
977	3kar		4	351	3.4e-66			185.54	KINESIN-LIKE PROTEIN KAR3; CHAIN: NULL;	CONTRACTILE PROTEIN KAR3, KINESIN-RELATED PROTEIN,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										MOTOR 2 PROTEIN, ATPASE, P-LOOP, MICROTUBULE BINDING PROTEIN
977	3kar		5	348	3.4e-66	0.58	1.00		KINESIN-LIKE PROTEIN KAR3; CHAIN: NULL;	CONTRACTILE PROTEIN, KINESIN-RELATED PROTEIN, MOTOR 2 PROTEIN, ATPASE, P-LOOP, MICROTUBULE BINDING PROTEIN
977	3kin	B	276	364	1.5e-34	-0.10	0.99		KINESIN HEAVY CHAIN; CHAIN: A, B, C, D;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
977	3kin	B	276	366	1e-16	-0.19	1.00		KINESIN HEAVY CHAIN; CHAIN: A, B, C, D;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
982	1aut	L	597	670	1.5e-10	0.03	-0.19		ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE, PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
982	1aut	L	745	823	1.1e-24	0.36	0.41		ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE, PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
982	1cej	A	740	820	1.9e-20	-0.11	0.16		MEROZOITE SURFACE PROTEIN 1; CHAIN: A;	SURFACE PROTEIN MEROZOITE SURFACE ANTIGEN 1, MAJOR BLOOD-STAGE EGF-LIKE DOMAIN, EXTRACELLULAR, MODULAR

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										PROTEIN, SURFACE 2 ANTIGEN, MALARIA VACCINE COMPONENT, SURFACE PROTEIN
982	1ckl	A	3	107	1.9e-16	0.22	0.17		CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
982	1d4v	A	556	658	5.7e-09	0.29	-0.12		TNF-RELATED APOPTOSIS INDUCING LIGAND; CHAIN: B; DEATH RECEPTOR 5; CHAIN: A;	APOPTOSIS TRAIL; DR5; LIGAND-RECEPTOR COMPLEX, TRIMERIC JELLY-ROLL, TNF-R 2 SUPERFAMILY, APOPTOSIS
982	1dan	L	738	823	6.8e-16	0.13	0.11		BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DFFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
982	1dan	L	741	831	1.1e-24	-0.19	0.27		BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DFFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
982	1dan	L	759	846	3.8e-24	-0.16	0.00		BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DFFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
982	1dva	L	734	831	3.8e-23	-0.18	0.00		DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	
982	1dva	L	738	823	6.8e-16	-0.02	0.13		DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
982	1e5g	A	3	96	3.8e-17	0.18	0.33		COMPLEMENT CONTROL PROTEIN; CHAIN: A;	COMPLEMENT INHIBITOR VCP, SP35; COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS
982	1emn		257	337	1.7e-11	0.09	-0.19		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
982	1emn		738	809	3.4e-15	-0.22	0.06		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
982	1ext	A	533	672	1.9e-10	0.07	0.01		TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	SIGNALING PROTEIN BINDING PROTEIN; CYTOKINE, SIGNALING PROTEIN
982	1f7e	A	741	781	5.7e-17	0.15	0.75		BLOOD COAGULATION FACTOR VII; CHAIN: A;	BLOOD CLOTTING FACTOR VII, BLOOD COAGULATION, EGF-LIKE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
982	1hfn		2	96	9.5e-16	0.03	0.23		GLYCOPROTEIN FACTOR H, 15TH AND 16TH C-MODULE PAIR (NMR, MINIMIZED 1HFHA 1 AVERAGED STRUCTURE) 1HFH 4 1HFHA 5	DOMAIN, BLOOD 2 CLOTTING
982	1pfx	L	741	840	1.3e-32	-0.03	0.11		FACTOR IXA; CHAIN: C, L; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
982	1qfk	L	741	830	3.8e-29	0.01	0.05		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
982	1wvc		2	96	1.7e-14	0.18	-0.09		VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR, SUSHI DOMAIN, 2 MODULE PAIR
982	1whe		744	814	1.1e-19	-0.30	0.11		COAGULATION FACTOR X; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN, HYDROLASE, SERINE PROTEASE, PLASMA, BLOOD 2 COAGULATION FACTOR
982	1xka	L	369	441	5.1e-10	0.04	-0.13		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
982	1xka	L	741	831	1.9e-27	0.05	0.06		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
982	4mt2		557	617	1.4e-09	-0.46	0.07		METALLOTHIONEIN METALLOTHIONEIN ISOFORM II 4MT2 3	
986	1a6a	B	22	202	1.4e-46			61.03	HLA-DR3; CHAIN: A, B; CLIP; CHAIN: C;	COMPLEX (TRANSMEMBRANE/GLYCOPROTEIN) MHC GLYCOPROTEIN, COMPLEX (TRANSMEMBRANE/GLYCOPROTEIN)
986	1a6a	B	25	201	1.4e-46	-0.06	0.39		HLA-DR3; CHAIN: A, B; CLIP; CHAIN: C;	COMPLEX (TRANSMEMBRANE/GLYCOPROTEIN) MHC GLYCOPROTEIN, COMPLEX (TRANSMEMBRANE/GLYCOPROTEIN)
986	1aqd	B	16	201	1.4e-46			57.96	HLA-DR1 CLASS II HISTOCOMPATIBILITY PROTEIN; CHAIN: A, B, D, E, G, H, J, K; HLA-A2; CHAIN: C, F, I, L;	COMPLEX (MHC PROTEIN/ANTIGEN) DRA, DRB1 01010; COMPLEX (MHC PROTEIN/ANTIGEN), HISTOCOMPATIBILITY ANTIGEN
986	1aqd	B	45	201	1.4e-46	-0.34	0.58		HLA-DR1 CLASS II HISTOCOMPATIBILITY PROTEIN; CHAIN: A, B, D, E, G, H, J, K; HLA-A2; CHAIN: C, F, I, L;	COMPLEX (MHC PROTEIN/ANTIGEN) DRA, DRB1 01010; COMPLEX (MHC PROTEIN/ANTIGEN), HISTOCOMPATIBILITY ANTIGEN
986	1bx2	A	22	202	8.5e-61			95.88	HLA-DR2; CHAIN: A, D; HLA-DR2; CHAIN: B, E; HLA-DR2; CHAIN: C, F;	IMMUNE SYSTEM HLA-DR2, MYELIN BASIC PROTEIN, MULTIPLE SCLEROSIS, 2 AUTOIMMUNITY, IMMUNE SYSTEM
986	1bx2	A	28	202	8.5e-61	-0.11	0.58		HLA-DR2; CHAIN: A, D; HLA-	IMMUNE SYSTEM HLA-DR2,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									DR2; CHAIN: B, E; HLA-DR2; CHAIN: C, F;	MYELIN BASIC PROTEIN, MULTIPLE SCLEROSIS, 2 AUTOIMMUNITY, IMMUNE SYSTEM
986	1bx2	B	20	204	1.7e-45			59.12	HLA-DR2; CHAIN: A, D; HLA-DR2; CHAIN: B, E; HLA-DR2; CHAIN: C, F;	IMMUNE SYSTEM HLA-DR2, MYELIN BASIC PROTEIN, MULTIPLE SCLEROSIS, 2 AUTOIMMUNITY, IMMUNE SYSTEM
986	1bx2	B	45	201	1.7e-45	-0.39	0.46		HLA-DR2; CHAIN: A, D; HLA-DR2; CHAIN: B, E; HLA-DR2; CHAIN: C, F;	IMMUNE SYSTEM HLA-DR2, MYELIN BASIC PROTEIN, MULTIPLE SCLEROSIS, 2 AUTOIMMUNITY, IMMUNE SYSTEM
986	1fv1	A	29	202	3.4e-60	-0.31	0.90		MAJOR HISTOCOMPATIBILITY COMPLEX ALPHA CHAIN; CHAIN: A, D; MAJOR HISTOCOMPATIBILITY COMPLEX BETA CHAIN; CHAIN: B, E; MYELIN BASIC PROTEIN; CHAIN: C, F;	IMMUNE SYSTEM MHC CLASS II DR2A
986	1fv1	B	29	201	1.7e-46	-0.50	0.39		MAJOR HISTOCOMPATIBILITY COMPLEX ALPHA CHAIN; CHAIN: A, D; MAJOR HISTOCOMPATIBILITY COMPLEX BETA CHAIN; CHAIN: B, E; MYELIN BASIC PROTEIN; CHAIN: C, F;	IMMUNE SYSTEM MHC CLASS II DR2A
986	1hdm	A	20	207	3.4e-43			282.05	CLASS II HISTOCOMPATIBILITY ANTIGEN, M ALPHA CHAIN: A; CLASS II HISTOCOMPATIBILITY ANTIGEN, M BETA CHAIN: B;	IMMUNE SYSTEM RING6, HLA-DMA; RING7, HLA-DMB; HISTOCOMPATIBILITY PROTEIN, IMMUNE SYSTEM
986	1iak	A	20	202	1e-61			106.84	MHC CLASS II I-AK; CHAIN: A, B, P; HEN EGGWHITE LYSOZYME PEPTIDE	HISTOCOMPATIBILITY ANTIGEN I-AK HISTOCOMPATIBILITY ANTIGEN, MHC, PEPTIDE COMPLEX

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
986	liak	A	37	202	1e-61	-0.12	1.00		MHC CLASS II I-AK; CHAIN: A, B; P; HEN EGGWHITE LYSOZYME PEPTIDE	HISTOCOMPATIBILITY ANTIGEN I-AK HISTOCOMPATIBILITY ANTIGEN, MHC, PEPTIDE COMPLEX
986	liak	B	23	201	1.5e-43			59.46	MHC CLASS II I-AK; CHAIN: A, B; P; HEN EGGWHITE LYSOZYME PEPTIDE	HISTOCOMPATIBILITY ANTIGEN I-AK HISTOCOMPATIBILITY ANTIGEN, MHC, PEPTIDE COMPLEX
986	liao	B	1	201	1.2e-43			58.50	MHC CLASS II I-AD; CHAIN: A, B;	MHC II MHC II, CLASS II MHC, I-A, OVALBUMIN PEPTIDE
986	liea	A	21	203	5.1e-59			100.86	MHC CLASS II I-EK; CHAIN: A, B, C, D;	HISTOCOMPATIBILITY ANTIGEN HISTOCOMPATIBILITY ANTIGEN
986	liea	A	27	203	5.1e-59	-0.28	0.95		MHC CLASS II I-EK; CHAIN: A, B, C, D;	HISTOCOMPATIBILITY ANTIGEN HISTOCOMPATIBILITY ANTIGEN
986	liea	B	2	199	3.4e-45			53.16	MHC CLASS II I-EK; CHAIN: A, B, C, D;	HISTOCOMPATIBILITY ANTIGEN HISTOCOMPATIBILITY ANTIGEN
986	lieb	B	1	199	3.4e-45			58.75	MHC CLASS II I-EK; CHAIN: A, B, C, D;	HISTOCOMPATIBILITY ANTIGEN HISTOCOMPATIBILITY ANTIGEN
986	lieb	B	51	199	3.4e-45	-0.34	0.21		MHC CLASS II I-EK; CHAIN: A, B, C, D;	HISTOCOMPATIBILITY ANTIGEN HISTOCOMPATIBILITY ANTIGEN
986	2iad	A	20	207	3.4e-61			109.34	MHC CLASS II I-AD; CHAIN: A, B;	MHC II MHC II, CLASS II MHC I-AD
986	2iad	A	37	206	3.4e-61	0.09	1.00		MHC CLASS II I-AD; CHAIN: A, B;	MHC II MHC II, CLASS II MHC I-AD
986	2iad	B	2	201	3.4e-44			59.80	MHC CLASS II I-AD; CHAIN: A, B;	MHC II MHC II, CLASS II MHC I-AD
987	1a4y	A	52	214	1.9e-11	-0.43	0.60		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS
987	1a9n	A	49	130	3.8e-15	-0.29	0.89		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
987	1a9n	A	52	199	3.8e-14	0.10	0.40		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	SNRNP, RIBONUCLEOPROTEIN COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
987	1a9n	C	49	145	3.8e-15	0.07	0.94		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
987	1a9n	C	52	199	5.7e-14	0.05	0.35		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
987	1c1g	A	231	493	5.1e-19	-0.72	0.03		TROPOMYOSIN; CHAIN: A, B, C, D	CONTRACTILE PROTEIN TROPOMYOSIN COILED-COIL ALPHA-HELICAL, CONTRACTILE PROTEIN
987	1d0b	A	5	162	1.2e-18	0.33	0.98		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
987	1dce	A	34	151	1.2e-14	0.27	0.66		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
987	1ds9	A	48	150	1e-14	-0.19	0.52		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
987	1ds9	A	50	155	3.8e-15	-0.08	0.55		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
987	1quu	A	236	491	7.6e-07			72.54	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CHLAMYDOMONAS, FLAGELLA CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
987	1yrg	A	57	210	1.9e-12	-0.14	0.13		GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	TRANSCRIPTION RNAIP; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPII, GTPASE-ACTIVATING PROTEIN, GAP, RNAIP, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
991	1qf8	A	7	123	3.8e-56	0.46	1.00		CASEIN KINASE II; CHAIN: A, B;	TRANSFERASE CASEIN KINASE BETA SUBUNIT (1-182), SER/THR
991	1qf8	A	7	123	6.8e-51	0.46	1.00		CASEIN KINASE II; CHAIN: A, B;	PROTEIN KINASE, 2 ZN FINGER
993	2occ	H	73	141	8.5e-29	0.10	0.07		CYTOCHROME C OXIDASE; CHAIN: A, B, C, D, E, F, G, H, I, J, K, L, M, N, O, P, Q;	TRANSFERASE CASEIN KINASE BETA SUBUNIT (1-182), SER/THR
994	1ddq	C	1	1076	0	-0.22	0.96		DNA-DIRECTED RNA POLYMERASE; CHAIN: A, B; DNA-DIRECTED RNA POLYMERASE; CHAIN: C; DNA-DIRECTED RNA POLYMERASE; CHAIN: D; DNA-DIRECTED	PROTEIN KINASE, 2 ZN FINGER
										OXIDOREDUCTASE FERROCYTOCHROME C:OXYGEN OXIDOREDUCTASE; OXIDOREDUCTASE, CYTOCHROME(C)-OXYGEN, CYTOCHROME C 2 OXIDASE
										TRANSCRIPTION TRANSFERASE, TRANSCRIPTION, DNA-DIRECTED RNA POLYMERASE, 3D- 2 STRUCTURE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									RNA POLYMERASE; CHAIN: E;	
995	1bor		2	50	1.4e-08	-0.39	0.05		TRANSCRIPTION FACTOR PML; CHAIN: NULL;	TRANSCRIPTION REGULATION PROTO-ONCOGENE, NUCLEAR BODIES (PODS), LEUKEMIA, 2 TRANSCRIPTION REGULATION
995	1chc		10	51	1.7e-12	0.29	0.59		VIRUS EQUINE HERPES VIRUS-1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	
995	1chc		6	60	5.7e-12	-0.45	0.47		VIRUS EQUINE HERPES VIRUS-1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	
995	1fbv	A	10	51	5.1e-10	-0.04	0.52		SIGNAL TRANSDUCTION PROTEIN CBL; CHAIN: A; ZAP-70 PEPTIDE; CHAIN: B; UBIQUITIN-CONJUGATING ENZYME E12-18 KDA UBCH7; CHAIN: C;	LIGASE CBL, UBCH7, ZAP-70, E2, UBIQUITIN, E3, PHOSPHORYLATION, 2 TYROSINE KINASE, UBIQUITINATION, PROTEIN DEGRADATION,
995	1fbv	A	9	60	3.8e-09	-0.46	0.30		SIGNAL TRANSDUCTION PROTEIN CBL; CHAIN: A; ZAP-70 PEPTIDE; CHAIN: B; UBIQUITIN-CONJUGATING ENZYME E12-18 KDA UBCH7; CHAIN: C;	LIGASE CBL, UBCH7, ZAP-70, E2, UBIQUITIN, E3, PHOSPHORYLATION, 2 TYROSINE KINASE, UBIQUITINATION, PROTEIN DEGRADATION,
995	1fre		98	134	3.4e-05	-0.11	0.03		NUCLEAR FACTOR XNF7; CHAIN: NULL;	ZINC-BINDING PROTEIN ZINC-BINDING PROTEIN, XNF7, BBOX, DEVELOPMENT, 3 MID-BLASTULA-TRANSITION
995	1g25	A	6	57	0.00017	-0.33	0.46		CDK-ACTIVATING KINASE ASSEMBLY FACTOR MAT1; CHAIN: A;	METAL BINDING PROTEIN RING FINGER PROTEIN MAT1; RING FINGER (C3HC4)
995	1rmd		4	100	1.1e-16	0.13	0.49		RAG1; CHAIN: NULL;	DNA-BINDING PROTEIN V(D)J

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										RECOMBINATION ACTIVATING PROTEIN 1; RAG1, V(D)J RECOMBINATION, ANTIBODY, MAD, RING FINGER, 2 ZINC BINUCLEAR CLUSTER, ZINC FINGER, DNA-BINDING PROTEIN
996	1am9	B	277	345	7.6e-09	-0.25	0.01		STEROL REGULATORY ELEMENT BINDING PROTEIN 1A; CHAIN: A, B, C, D; DNA; CHAIN: E, F, G, H;	COMPLEX (TRANSCRIPTION REGULATION/DNA) SREBP-1A; STEROL REGULATORY ELEMENT BINDING PROTEIN, 2 BASIC-HELIX-LOOP-HELIX-LEUCINE ZIPPER, SREBP, TRANSCRIPTION 3 FACTOR, COMPLEX (TRANSCRIPTION REGULATION/DNA)
996	1an2	A	277	354	3.8e-15	-0.60	0.01		MAX PROTEIN; CHAIN: A, C; DNA; CHAIN: B, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) MYN PROTEIN; MAX, DNA BINDING, BASIC-HELIX-LOOP-HELIX-LEUCINE ZIPPER, 2 TRANSCRIPTION FACTOR, COMPLEX (DNA-BINDING PROTEIN/DNA)
996	1hlo	A	268	343	1.9e-13	-0.26	0.10		TRANSCRIPTION FACTOR MAX; CHAIN: A, B; DNA (5'-D(*CP*AP*CP*CP*AP*CP*GP*T P*GP*GP*T)-3', CHAIN: C, D;	COMPLEX (TRANSCRIPTION FACTOR MAX/DNA) TRANSCRIPTIONAL REGULATION, DNA BINDING, COMPLEX 2 (TRANSCRIPTION FACTOR MAX/DNA)
996	1hlo	B	277	343	1.9e-12	-0.32	0.19		TRANSCRIPTION FACTOR MAX; CHAIN: A, B; DNA (5'-D(*CP*AP*CP*CP*AP*CP*GP*T P*GP*GP*T)-3', CHAIN: C, D;	COMPLEX (TRANSCRIPTION FACTOR MAX/DNA) TRANSCRIPTIONAL REGULATION, DNA BINDING, COMPLEX 2 (TRANSCRIPTION FACTOR MAX/DNA)

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
997	1byu	A	17	139	5.1e-46	-0.02	0.64		GTP-BINDING PROTEIN RAN; CHAIN: A, B;	TRANSPORT PROTEIN TC4; GTPASE, NUCLEAR TRANSPORT, TRANSPORT PROTEIN
997	1byu	B	13	139	1.2e-46	0.17	0.72		GTP-BINDING PROTEIN RAN; CHAIN: A, B;	TRANSPORT PROTEIN TC4; GTPASE, NUCLEAR TRANSPORT, TRANSPORT PROTEIN
997	1cc0	A	23	140	3.4e-47	-0.23	0.96		TRANSFORMING PROTEIN RHOA; CHAIN: A, C; RHO GDP DISSOCIATION INHIBITOR ALPHA; CHAIN: E, F;	SIGNALING PROTEIN GTP-BINDING PROTEIN RHOA, GTPASE RHOA; RHO GDI 1; RHO GTPASE, G-PROTEIN, SIGNALING PROTEIN
997	1cxz	A	23	140	1e-47	-0.14	0.98		HIS-TAGGED TRANSFORMING PROTEIN RHOA(0-181); CHAIN: A; PKN; CHAIN: B;	SIGNALING PROTEIN PROTEIN-PROTEIN COMPLEX, ANTIPARALLEL COILED-COIL
997	1d5c	A	22	143	1.4e-49	0.14	0.84		RAB6 GTPASE; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS G-PROTEIN, GTPASE, RAB6, VESICULAR TRAFFICKING
997	1ds6	A	22	140	8.5e-49	-0.05	0.88		RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 2; CHAIN: A; RHO GDP-DISSOCIATION INHIBITOR 2; CHAIN: B;	SIGNALING PROTEIN P21-RAC2; RHO GDI 2, RHO-GDI BETA, LY-GDI; BETA SANDWHICH, PROTEIN-PROTEIN COMPLEX, G-DOMAIN, 2 IMMUNOGLOBULIN FOLD, WALKER FOLD, GTP-BINDING PROTEIN
997	1ibr	A	20	145	1.4e-45			68.78	RAN; CHAIN: A, C; IMPORTIN BETA SUBUNIT; CHAIN: B, D;	SMALL GTPASE KARYOPHERIN BETA, P95 SMALL GTPASE, NUCLEAR TRANSPORT RECEPTOR
997	1mh1		17	145	5.1e-50			52.24	RAC1; CHAIN: NULL;	GTP-BINDING GTP-BINDING, GTPASE, SMALL G-PROTEIN, RHO FAMILY, RAS SUPER 2 FAMILY
997	1mh1		22	140	5.1e-50	-0.12	0.87		RAC1; CHAIN: NULL;	GTP-BINDING GTP-BINDING, GTPASE, SMALL G-PROTEIN, RHO FAMILY, RAS SUPER 2 FAMILY
997	1rrp	C	19	145	1.4e-45			65.13	RAN; CHAIN: A, C; NUCLEAR	COMPLEX (SMALL

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									PORE COMPLEX PROTEIN NUP358; CHAIN: B; D;	GTPASE/NUCLEAR PROTEIN) COMPLEX (SMALL GTPASE/NUCLEAR PROTEIN), SMALL GTPASE, 2 NUCLEAR TRANSPORT
997	1zbd	A	17	144	1.7e-53			54.15	RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;	COMPLEX (GTP-BINDING/EFFECTOR) RAS-RELATED PROTEIN RAB3A; COMPLEX (GTP-BINDING/EFFECTOR), G PROTEIN, EFFECTOR, RABCDR, 2 SYNAPTIC EXOCYTOSIS, RAB PROTEIN, RAB3A, RABPHILIN
997	1zbd	A	18	143	1.7e-53	0.17	0.78		RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;	COMPLEX (GTP-BINDING/EFFECTOR) RAS-RELATED PROTEIN RAB3A; COMPLEX (GTP-BINDING/EFFECTOR), G PROTEIN, EFFECTOR, RABCDR, 2 SYNAPTIC EXOCYTOSIS, RAB PROTEIN, RAB3A, RABPHILIN
997	2ngr	A	22	141	3.4e-46	-0.07	0.89		GTP BINDING PROTEIN (G25K); CHAIN: A; GTPASE ACTIVATING PROTEIN (RHG); CHAIN: B;	HYDROLASE CDC42/CDC42GAP; CDC42/CDC42GAP; TRANSITION STATE, G-PROTEIN, GAP, CDC42, ALF3, HYDROLASE
997	3rab	A	17	143	5.1e-55	0.19	0.88		RAB3A; CHAIN: A;	HYDROLASE G PROTEIN, VESICULAR TRAFFICKING, GTP HYDROLYSIS, RAB 2 PROTEIN, NEUROTRANSMITTER RELEASE, HYDROLASE
997	3rab	A	17	145	5.1e-55			64.11	RAB3A; CHAIN: A;	HYDROLASE G PROTEIN, VESICULAR TRAFFICKING, GTP HYDROLYSIS, RAB 2 PROTEIN, NEUROTRANSMITTER RELEASE, HYDROLASE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
998	1a06		1	174	1.7e-50	-0.20	0.16		CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE; CHAIN: NULL;	KINASE KINASE, SIGNAL TRANSDUCTION, CALCIUM/CALMODULIN
998	1apm	E	1	175	5.1e-66	-0.21	0.53		TRANSFERASE(PHOSPHOTRANSFERASE) \$C\$-AMP-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (\$C\$/APK\$) 1APM 3 (CATALYTIC SUBUNIT) ALPHA ISOENZYME MUTANT WITH SER 139 1APM 4 REPLACED BY ALA (\$S139A\$) COMPLEX WITH THE PEPTIDE 1APM 5 INHIBITOR PKI(5-24) AND THE DETERGENT MEGA-8 1APM 6	
998	1cmk	E	1	175	5.1e-66	-0.17	0.47		PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT 1CMK 3 (E.C.2.7.1.37) 1CMK 4	
998	1cip	E	1	161	1.2e-60	-0.02	0.78		TRANSFERASE(PHOSPHOTRANSFERASE) CAMP-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) ICTP 3 (CATALYTIC SUBUNIT) ICTP 4	
998	1f3m	C	1	160	3.4e-53	-0.02	0.51		SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA; CHAIN: A, B; SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA; CHAIN: C, D;	TRANSFERASE KINASE DOMAIN, AUTOINHIBITORY FRAGMENT, HOMODIMER
998	1koa		1	169	1.2e-38	-0.02	0.37		TWITCHIN; CHAIN: NULL;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
998	1kob	A	1	169	1.2e-40	-0.02	0.72		TWITCHIN; CHAIN: A, B;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
998	1phk		1	140	3.4e-54	0.13	0.80		PHOSPHORYLASE KINASE; CHAIN: NULL;	KINASE RABBIT MUSCLE PHOSPHORYLASE KINASE;

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										GLYCOGEN METABOLISM, TRANSFERASE, SERINE/THREONINE-PROTEIN, 2 KINASE, ATP-BINDING, CALMODULIN-BINDING
998	1tki	A	1	149	1.7e-34	0.18	0.75		TITIN; CHAIN: A, B;	SERINE KINASE SERINE KINASE, TITIN, MUSCLE, AUTOINHIBITION
998	1tki	A	1	186	1.9e-34	-0.12	0.25		TITIN; CHAIN: A, B;	SERINE KINASE SERINE KINASE, TITIN, MUSCLE, AUTOINHIBITION
1000	1bih	A	10	283	1.7e-27	0.28	0.40		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1000	1cs6	A	29	283	3.4e-34	0.09	0.10		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1000	1cvs	C	21	199	3.4e-25	0.08	0.15		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1000	1cvs	D	112	284	5.1e-36	0.15	0.21		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1000	1cvs	D	21	199	1.2e-26	0.03	-0.03		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1000	1epf	A	123	282	3.4e-18	0.11	-0.13		NEURAL CELL ADHESION	CELL ADHESION NCAM; NCAM,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									MOLECULE; CHAIN: A, B, C, D;	IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1000	1epf	A	33	201	3.4e-24	0.11	-0.09		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1000	1f2q	A	117	281	1.7e-19	0.12	0.31		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A;	IMMUNE SYSTEM FC-EPSILON R-ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN
1000	1f2q	A	28	208	3.4e-28	0.00	0.22		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A;	IMMUNE SYSTEM FC-EPSILON R-ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN
1000	1f6a	A	116	281	1e-17	0.31	0.57		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IG EPSILON CHAIN C REGION; CHAIN: B, D;	IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FCEPSILON IGE-FC; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC
1000	1f6a	A	26	207	1.4e-27	-0.04	0.12		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IG EPSILON CHAIN C REGION; CHAIN: B, D;	IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FCEPSILON IGE-FC; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC
1000	1fcg	A	115	281	1.7e-19	0.15	-0.12		FC RECEPTOR FC(GAMMA)RIIA; CHAIN: A;	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32; FC RECEPTOR, IMMUNOGLOULIN, LEUKOCYTE, CD32
1000	1fcg	A	26	205	5.1e-29	0.23	0.41		FC RECEPTOR FC(GAMMA)RIIA; CHAIN: A;	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32; FC RECEPTOR, IMMUNOGLOULIN, LEUKOCYTE, CD32
1000	1fnl	A	114	281	3.4e-17	0.05	0.06		LOW AFFINITY	IMMUNE SYSTEM RECEPTOR BETA

SEQ ID NO;	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									IMMUNOGLOBULIN GAMMA FC REGION CHAIN: A;	SANDWICH, IMMUNOGLOBULIN-LIKE, RECEPTOR
1000	1fml	A	24	206	1.5e-24	0.07	0.58		LOW AFFINITY IMMUNOGLOBULIN GAMMA FC REGION CHAIN: A;	IMMUNE SYSTEM RECEPTOR BETA SANDWICH, IMMUNOGLOBULIN-LIKE, RECEPTOR
1000	lkoa		207	284	5.1e-12	0.35	0.33		TWITCHIN; CHAIN: NULL;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
1000	lnct		213	284	3.4e-13	0.47	-0.15		TITIN; CHAIN: NULL;	MUSCLE PROTEIN CONNECTIN, NEXTIN5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN; 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN
1000	lnkr		117	282	3.4e-29	0.20	0.76		P58-CL42 KIR; CHAIN: NULL;	INHIBITORY RECEPTOR KILLER CELL INHIBITORY RECEPTOR; INHIBITORY RECEPTOR, NATURAL KILLER CELLS, IMMUNOLOGICAL 2 RECEPTORS, IMMUNOGLOBULIN FOLD
1000	lnkr		12	113	6.8e-13	-0.51	0.22		P58-CL42 KIR; CHAIN: NULL;	INHIBITORY RECEPTOR KILLER CELL INHIBITORY RECEPTOR; INHIBITORY RECEPTOR, NATURAL KILLER CELLS, IMMUNOLOGICAL 2 RECEPTORS, IMMUNOGLOBULIN FOLD
1000	lnkr		27	216	1e-30			71.59	P58-CL42 KIR; CHAIN: NULL;	INHIBITORY RECEPTOR KILLER CELL INHIBITORY RECEPTOR; INHIBITORY RECEPTOR, NATURAL KILLER CELLS, IMMUNOLOGICAL 2 RECEPTORS, IMMUNOGLOBULIN FOLD
1000	lnkr		28	204	1e-30	0.22	0.87		P58-CL42 KIR; CHAIN: NULL;	INHIBITORY RECEPTOR KILLER CELL INHIBITORY RECEPTOR;

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										INHIBITORY RECEPTOR, NATURAL KILLER CELLS, IMMUNOLOGICAL 2 RECEPTORS, IMMUNOGLOBULIN FOLD
1000	1nm		213	284	3.4e-13	0.37	-0.18		MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) 1TNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) 1TNM 4 1TNM 58	
1000	1yuh	H	28	236	8.5e-07			54.09	FAB FRAGMENT; CHAIN: NULL;	IMMUNOGLOBULIN ANTI-NITROPHENOL, LAMBDA LIGHT CHAIN, IMMUNOGLOBULIN
1000	2dli	A	117	282	3.4e-29	0.22	0.51		MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	IMMUNE SYSTEM P58 NATURAL KILLER CELL RECEPTOR; KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN
1000	2dli	A	26	203	5.1e-29	0.23	0.74		MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	IMMUNE SYSTEM P58 NATURAL KILLER CELL RECEPTOR; KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN
1000	2fcb	A	115	281	5.1e-20	0.26	-0.08		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
1000	2fcb	A	26	206	3.4e-29	0.03	0.55		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
1001	1d5r	A	291	344	0.0019	-0.64	0.07		PHOSPHOINOSITIDE PHOSPHOTASE PTEN; CHAIN: A;	HYDROLASE C2 DOMAIN, PHOSPHOTIDYLINOSITOL, PHOSPHOTASE, HYDROLASE
1003	1d5r	A	209	262	0.0019	-0.64	0.07		PHOSPHOINOSITIDE PHOSPHOTASE PTEN; CHAIN: A;	HYDROLASE C2 DOMAIN, PHOSPHOTIDYLINOSITOL, PHOSPHOTASE, HYDROLASE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1004	1d5r	A	291	344	0.0019	-0.64	0.07		PHOSPHONOSITIDE PHOSPHOTASE PTEN; CHAIN: A;	HYDROLASE C2 DOMAIN, PHOSPHOTIDYLINOSITOL, PHOSPHOTASE, HYDROLASE
1010	1cun	A	164	396	5.7e-16	0.04	-0.03		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1010	1cun	A	213	429	1.5e-16	-0.08	0.13		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1010	1cun	A	293	505	1.7e-13	-0.12	0.23		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1010	1dnl	B	236	470	5.7e-18	-0.32	0.01		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
1010	1ecr	A	61	288	0.0013	-0.61	0.00		REPLICATION TERMINATOR PROTEIN; CHAIN: A; DNA 16MER DUPLEX REPLICATION TERMINATOR; CHAIN: B, C;	COMPLEX (DNA-BINDING PROTEIN/DNA)
1010	1fio	A	133	329	3.8e-11	0.00	0.00		SSO1 PROTEIN; CHAIN: A;	MEMBRANE PROTEIN FOUR HELIX BUNDLE, ALPHA HELIX
1010	1fio	A	217	401	7.6e-11	0.02	-0.12		SSO1 PROTEIN; CHAIN: A;	MEMBRANE PROTEIN FOUR HELIX BUNDLE, ALPHA HELIX
1010	1quu	A	75	370	1.1e-22	-0.31	0.05		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										CONTRACTILE PROTEIN
1013	1dfn	A	109	138	1.1e-12			59.97	DEFENSIN DEFENSIN /HNP\$-3 IDFN 3	
1013	1dfn	A	110	138	1.1e-12	-0.35	1.00		DEFENSIN DEFENSIN /HNP\$-3 IDFN 3	
1013	1dfn	A	110	138	3.4e-11	-0.35	1.00		DEFENSIN DEFENSIN /HNP\$-3 IDFN 3	
1014	1cii		14	636	5.7e-59			148.75	COLICIN IA; CHAIN: NULL;	TRANSMEMBRANE PROTEIN COLICIN, BACTERIOCIN, ION CHANNEL FORMATION, TRANSMEMBRANE 2 PROTEIN
1014	1cun	A	190	394	3.8e-15	0.12	-0.09		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1014	1cun	A	218	447	1.9e-15	0.06	0.17		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1014	1cun	A	345	583	3.8e-21	0.11	0.04		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1014	1cun	A	419	634	1.9e-19	0.44	-0.02		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1014	1cun	A	50	284	1.9e-09	-0.09	0.30		ALPHA SPECTRIN; CHAIN: A,	STRUCTURAL PROTEIN TWO

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									B, C;	REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1014	1cun	A	525	741	5.7e-10	-0.06	0.12		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1014	1dg3	A	55	307	0.0057	-0.16	0.17		INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1; CHAIN: A;	SIGNALING PROTEIN GUANINE NUCLEOTIDE-BINDING PROTEIN 1; GBP, GTP HYDROLYSIS, GDP, GMP, INTERFERON INDUCED, DYNAMIN 2 RELATED, LARGE GTPASE FAMILY, SIGNALING PROTEIN
1014	1dn1	B	297	509	1.5e-18	0.07	-0.07		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
1014	1dn1	B	370	598	5.7e-26	-0.04	0.23		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
1014	1dn1	B	484	733	1.7e-09	0.02	0.66		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
1014	1fio	A	361	518	1.9e-11	0.01	-0.17		SSO1 PROTEIN; CHAIN: A;	MEMBRANE PROTEIN FOUR HELIX BUNDLE, ALPHA HELIX
1014	1fxk	C	308	422	1.9e-05	0.08	0.01		PREFOLDIN; CHAIN: A; PREFOLDIN; CHAIN: B; PREFOLDIN; CHAIN: C;	CHAPERONE ARCHAEAL PROTEIN
1014	1fxk	C	391	513	3.8e-07	0.00	0.15		PREFOLDIN; CHAIN: A; PREFOLDIN; CHAIN: B; PREFOLDIN; CHAIN: C;	CHAPERONE ARCHAEAL PROTEIN
1014	1fxk	C	472	578	1.9e-05	0.26	0.22		PREFOLDIN; CHAIN: A; PREFOLDIN; CHAIN: B;	CHAPERONE ARCHAEAL PROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1014	1fxk	C	552	635	0.00057	0.21	0.11		PREFOLDIN; CHAIN: C; PREFOLDIN; CHAIN: A; PREFOLDIN; CHAIN: B; PREFOLDIN; CHAIN: C;	CHAPERONE ARCHAEAL PROTEIN
1014	1quu	A	272	549	1.1e-24	0.15	0.07		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
1014	1quu	A	321	580	1.3e-32	0.48	0.01		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
1014	1quu	A	359	630	7.6e-27	0.20	0.15		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
1014	1quu	A	471	746	3.8e-17	-0.05	0.03		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
1014	1quu	A	81	398	3.8e-15	-0.06	0.03		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
1015	1alh	A	349	429	1.2e-23	-0.31	0.62		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1015	1alh	A	378	468	1.7e-24	0.01	-0.06		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1015	1alh	A	405	498	1.7e-26	0.11	0.03		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1015	1alh	A	472	555	1e-27	-0.37	0.28		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA),

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	ZINC FINGER, DNA-BINDING PROTEIN
1015	1alh	A	901	981	3.4e-30	0.34	0.10		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1015	1alh	A	929	1010	3.4e-30	0.10	0.87		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1015	1bbo		505	554	1.7e-10	-0.65	0.18		DNA-BINDING PROTEIN HUMAN ENHANCER-BINDING PROTEIN MBP-1 MUTANT WITH CYS 111 BB0 3 REPLACED BY ABU (C111ABU) (NMR, 60 STRUCTURES) BB0 4	
1015	Imey	C	349	429	1.7e-41	-0.12	0.81		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1015	Imey	C	374	468	1.7e-42	-0.01	0.72		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1015	Imey	C	404	496	1.7e-45	-0.01	0.82		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1015	Imey	C	443	527	5.1e-47	-0.25	0.95		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1015	Imey	C	471	556	3.4e-46	-0.26	0.90		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1015	Imey	C	530	612	1.5e-36	0.01	-0.14		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1015	Imey	C	698	778	6.8e-44	0.02	-0.20		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1015	Imey	C	840	953	5.1e-45	0.12	-0.15		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1015	Imey	C	901	981	3.4e-50	0.25	0.51		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1015	Imey	C	928	1010	3.4e-50	-0.07	0.88		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1015	Imey	G	500	527	3.4e-12	-0.05	0.39		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1015	1mey	G	528	556	5.1e-11	-0.71	0.24		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1015	1mey	G	839	865	1.5e-11	0.22	-0.18		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1015	1mey	G	926	953	1e-12	-0.03	0.42		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1015	1mey	G	982	1010	8.5e-12	0.23	0.65		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1015	1paa		985	1013	1.7e-05	-0.38	0.96		TRANSCRIPTION REGULATION YEAST TRANSCRIPTION FACTOR ADR1 (RESIDUES 130 - 159) IPAA 3 (PAPA - CARBOXY TERMINAL ZINC FINGER DOMAIN) MUTANT WITH IPAA 4 PRO 131 REPLACED BY ALA, PRO 133 REPLACED BY ALA, CYS 140 IPAA 5 REPLACED BY ALA (P131A,P133A,C140A)	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1015	1sp1		985	1010	0.00051	-0.10	0.70		(NMR, 10 STRUCTURES) IPAA 6 SP1F3; CHAIN: NULL;	ZINC FINGER TRANSCRIPTION FACTOR SP1; ZINC FINGER, TRANSCRIPTION ACTIVATION, SP1
1015	1sp2		349	375	0.00017	-0.77	0.27		SP1F2; CHAIN: NULL;	ZINC FINGER TRANSCRIPTION FACTOR SP1; ZINC FINGER, TRANSCRIPTION ACTIVATION, SP1
1015	1sp2		985	1010	1.9e-05	-0.54	0.90		SP1F2; CHAIN: NULL;	ZINC FINGER TRANSCRIPTION FACTOR SP1; ZINC FINGER, TRANSCRIPTION ACTIVATION, SP1
1015	1tf3	A	377	468	6.8e-17	-0.11	0.05		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
1015	1tf3	A	405	496	3.4e-18	0.15	0.23		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
1015	1tf3	A	472	551	1.7e-18	-0.17	0.03		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1015	1tf3	A	929	1010	1.5e-21	-0.17	0.64		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
1015	1tf6	A	405	565	8.5e-34	-0.42	0.47		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1015	1tf6	A	472	593	1.7e-28	-0.65	0.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1015	1ubd	C	351	496	7.6e-17	-0.56	0.29		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1015	1ubd	C	354	468	8.5e-31	-0.39	0.28		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1015	1ubd	C	384	497	1.7e-31	-0.13	0.47		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1015	1ubd	C	412	527	5.1e-30	-0.38	0.54		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1015	1ubd	C	479	584	1e-31	-0.26	0.57		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1015	1ubd	C	813	953	6.8e-28	0.04	-0.18		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)

SEQ ID NO:	PDB ID	CHAI NID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										(TRANSCRIPTION REGULATION/DNA)
1015	1ubd	C	848	981	3.4e-30	0.13	0.00		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1015	1ubd	C	908	1006	3.4e-34	0.22	0.84		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1015	1ubd	C	933	1086	5.1e-27	-0.56	0.81		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1015	2adr		349	403	6.8e-12	-0.66	0.19		ADRI; CHAIN: NULL;	TRANSCRIPTION REGULATION, TRANSCRIPTION REGULATION, ADRI, ZINC FINGER, NMR
1015	2adr		503	558	8.5e-15	-0.80	0.39		ADRI; CHAIN: NULL;	TRANSCRIPTION REGULATION, TRANSCRIPTION REGULATION, ADRI, ZINC FINGER, NMR
1015	2adr		901	955	3.4e-16	0.39	0.09		ADRI; CHAIN: NULL;	TRANSCRIPTION REGULATION, TRANSCRIPTION REGULATION,

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1015	2adr		957	1015	6.8e-18	-0.01	0.80		ADRI; CHAIN: NULL;	ADRI, ZINC FINGER, NMR
1015	2drp	A	372	428	3.4e-06	-0.30	0.11		COMPLEX(TRANSCRIPTION REGULATION/DNA) TRAMTRACK PROTEIN (TWO ZINC-FINGER PEPTIDE) COMPLEXED WITH 2DRP 3 DNA 2DRP 4	TRANSCRIPTION REGULATION, ADRI, ZINC FINGER, NMR
1015	2drp	A	501	556	8.5e-10	-0.47	0.01		COMPLEX(TRANSCRIPTION REGULATION/DNA) TRAMTRACK PROTEIN (TWO ZINC-FINGER PEPTIDE) COMPLEXED WITH 2DRP 3 DNA 2DRP 4	
1015	2gli	A	354	428	3.4e-18	-0.36	0.21		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1015	2gli	A	358	467	1.5e-26	-0.44	0.10		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1015	2gli	A	404	556	6.8e-33	-0.34	0.71		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1015	2gli	A	451	583	8.5e-33	-0.29	0.28		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1015	2gli	A	479	593	5.1e-28	-0.67	0.15		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI;

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1015	2gli	A	901	1010	1e-33	-0.18	0.96		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1015	7znf		985	1013	3.4e-05	-0.23	0.31		ZINC FINGER DNA BINDING DOMAIN ZINC-FINGER (ZFY-SWAP) (NMR, 12 STRUCTURES) 7ZNF 3	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1021	2occ	A	1	299	3.4e-88	0.01	-0.17		CYTOCHROME C OXIDASE; CHAIN: A, B, C, D, E, F, G, H, I, J, K, L, M, N, O, P, Q;	OXIDOREDUCTASE FERROCYTOCHROME C:OXYGEN OXIDOREDUCTASE; OXIDOREDUCTASE, CYTOCHROME(C)-OXYGEN, CYTOCHROME C 2 OXIDASE
1023	1amu	A	48	610	0			139.53	GRAMICIDIN SYNTHETASE I; CHAIN: A, B; PHENYLALANINE; CHAIN: C, D;	PEPTIDE SYNTHETASE GRSA; PEPTIDE SYNTHETASE, GRSA, ADENYLATE FORMING
1023	1lei		59	608	0			133.28	LUCIFERASE; CHAIN: NULL;	OXIDOREDUCTASE OXIDOREDUCTASE, MONOOXYGENASE, PHOTOPROTEIN, LUMINESCENCE
1028	1alh	A	98	184	3.4e-29			76.54	QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1028	1mey	C	157	239	1.7e-50			97.35	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1028	1hf6	A	97	269	1.4e-36			106.38	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1028	1ubd	C	130	239	6.8e-35			87.68	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1028	2gli	A	99	240	3.4e-31			87.54	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1029	1bih	A	1	351	6.8e-48			65.92	HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1029	1cap	B	133	348	1.7e-10			55.72	CATALYTIC ANTIBODY 17E8 COMPLEXED WITH PHENYL [1-(1-N-SUCCINYLAMINO)PENTYL] LEAP 3 PHOSPHONATE LEAP 4	
1029	1itb	B	54	353	1.7e-34			51.71	INTERLEUKIN-1 BETA; CHAIN: A; TYPE 1 INTERLEUKIN-1 RECEPTOR; CHAIN: B;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE,

SEQ ID NO;	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR)
1029	1kb5	H	133	351	1.7e-08			59.81	KB5-C20 T-CELL ANTIGEN RECEPTOR; CHAIN: A, B; ANTIBODY DESIRE-1; CHAIN: L, H;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) TCR VAPLHA VBETA DOMAIN; T-CELL RECEPTOR, STRAND SWITCH, FAB, ANTICLONOTYPIC, 2 (IMMUNOGLOBULIN/RECEPTOR)
1029	1mam	H	139	349	1.2e-11			56.22	IMMUNOGLOBULIN ANTIGEN-BINDING FRAGMENT (FAB) (IGG2B, KAPPA) IMAM 3	
1031	1uby		57	398	5.1e-66	-0.31	0.11		FARNESYL DIPHOSPHATE SYNTHASE; CHAIN: NULL;	TRANSFERASE FPS; TRANSFERASE, ISOPRENE BIOSYNTHESIS, CHOLESTEROL BIOSYNTHESIS
1031	1uby		65	397	5.1e-66			70.74	FARNESYL DIPHOSPHATE SYNTHASE; CHAIN: NULL;	TRANSFERASE FPS; TRANSFERASE, ISOPRENE BIOSYNTHESIS, CHOLESTEROL BIOSYNTHESIS
1032	1dfn	A	132	161	1.1e-12			58.55	DEFENSIN DEFENSIN /HNP\$-3 IDFN 3	
1032	1dfn	A	133	161	1.1e-12	-0.35	1.00		DEFENSIN DEFENSIN /HNP\$-3 IDFN 3	
1032	1dfn	A	133	161	5.1e-11	-0.35	1.00		DEFENSIN DEFENSIN /HNP\$-3 IDFN 3	
1034	1a4y	A	66	224	5.7e-22	-0.15	0.35		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE); COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS
1034	1a9n	A	68	208	3.8e-24	0.44	0.78		U2 RNA HAIRPIN IV; CHAIN: Q;	COMPLEX (NUCLEAR

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	PROTEIN/RNA COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1034	1a9n	A	93	249	1.3e-21	0.15	0.57		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1034	1a9n	C	68	208	1.1e-23	0.52	0.80		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1034	1a9n	C	93	249	9.5e-21	0.21	0.62		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1034	1cs6	A	279	363	3.8e-06	0.12	0.05		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1034	1cvs	C	283	364	7.6e-07	0.27	0.22		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1034	1cvs	D	283	367	1.5e-06	0.15	0.25		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1034	1d0b	A	39	186	8.5e-19	0.22	0.74		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1034	1d0b	A	44	223	1.9e-24	0.13	0.58		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1034	1dce	A	106	218	1e-09	-0.25	0.03		RAB GERANYLGERANYLTRANSFERASE RASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE RASE BETA SUBUNIT; CHAIN: B, D;	ADHESION TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N- FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1034	1dce	A	38	235	1.9e-16	0.05	-0.01		RAB GERANYLGERANYLTRANSFERASE RASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE RASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N- FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1034	1ds9	A	104	245	1e-08	-0.76	0.10		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE- RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1034	1ds9	A	45	208	7.6e-21	-0.56	0.04		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE- RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1034	1epf	A	279	358	5.7e-07	0.10	0.98		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1034	1ev2	E	276	373	1.5e-06	0.15	0.33		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1034	1ev2	G	283	358	3.8e-06	0.12	0.77		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2;

SEQ ID NO:	PDB ID	CHAI NID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1034	1fo1	A	183	230	0.0013	-0.40	0.25		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1034	1fo1	B	183	236	0.00076	-0.61	0.05		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1034	1tit		280	356	5.7e-06	0.21	0.01		TITIN, I27; CHAIN: NULL;	IMMUNOGLOBULIN-LIKE DOMAIN CONNECTIN I27, TITIN IG REPEAT 27; MUSCLE PROTEIN, IMMUNOGLOBULIN-LIKE DOMAIN
1034	1tnm		279	358	1.7e-06	0.23	0.34		MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) 1TNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) 1TNM 4 1TNM 58	
1034	1www	X	394	490	1.7e-09	0.25	-0.19		NERVE GROWTH FACTOR; CHAIN: V, W; TRKA RECEPTOR; CHAIN: X, Y;	NERVE GROWTH FACTOR/TRKA COMPLEX BETA-NGF; COMPLEX, TRKA RECEPTOR, NERVE GROWTH FACTOR, CYSTEINE KNOT, 2 IMMUNOGLOBULIN LIKE DOMAIN, NERVE GROWTH FACTOR/TRKA COMPLEX
1034	1yrg	A	44	198	7.6e-19	-0.34	0.24		GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	TRANSCRIPTION RNAIP; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPII, GTPASE-ACTIVATING PROTEIN, GAP, RNAIP, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										HEMIEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
1034	3ncm	A	279	358	9.5e-07	0.40	0.46		NEURAL CELL ADHESION MOLECULE, LARGE ISOFORM; CHAIN: A;	CELL ADHESION PROTEIN NCAM MODULE 2; CELL ADHESION, GLYCOPROTEIN, HEPARIN-BINDING, GPI-ANCHOR, 2 NEURAL ADHESION MOLECULE, IMMUNOGLOBULIN FOLD, HOMOPHILIC 3 BINDING, CELL ADHESION PROTEIN
1035	1cke	A	360	519	0.0019	-0.10	0.12		CYTIDINE MONOPHOSPHATE KINASE; CHAIN: A;	TRANSFERASE CK, MSSA; NUCLEOTIDE MONOPHOSPHATE KINASE, TRANSFERASE
1035	1coz	A	193	312	1.1e-11	0.18	0.18		GLYCEROL-3-PHOSPHATE CYTIDYL TRANSFERASE; CHAIN: A, B;	TRANSFERASE TRANSFERASE
1035	1d6j	A	359	393	1.9e-05	-0.55	0.35		ADENOSINE-5'PHOSPHOSULFATE KINASE; CHAIN: A, B;	TRANSFERASE APS KINASE; APS KINASE, ADENYLSULFATE KINASE, SULFATE, NUCLEOTIDE 2 KINASE, TRANSFERASE
1038	1eth	A	1	319	0			112.24	TRIACYLGLYCEROL ACYL-HYDROLASE; CHAIN: A, C; COLIPASE; CHAIN: B, D	COMPLEX (HYDROLASE/COFACTOR), LIPID DEGRADATION
1038	1gpl		2	316	0			107.65	RP2 LIPASE; CHAIN: NULL;	SERINE ESTERASE RELATED PROTEIN 2 LIPASE; SERINE ESTERASE, HYDROLASE, LIPID DEGRADATION, PANCREAS, 2 GLYCOPROTEIN, CHIMERIC

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1038	1hpl	A	1	318	0			107.77	HYDROLASE(CARBOXYLIC ESTERASE) LIPASE (E.C.3.1.1.3) (TRIACYLGLYCEROL HYDROLASE) 1HPL 3	
1038	1lpb	B	1	316	0			109.40	HYDROLASE(CARBOXYLIC ESTERASE) LIPASE (E.C.3.1.1.3) COMPLEXED WITH COLIPASE AND INHIBITED 1LPB 3 BY UNDECANE PHOSPHONATE METHYL ESTER (TWO CONFORMATIONS) 1LPB 4	
1038	1lrp1		2	316	0			100.01	PANCREATIC LIPASE RELATED PROTEIN 1; CHAIN: NULL;	HYDROLASE HYDROLASE, LIPID DEGRADATION, PANCREATIC LIPASE
1044	1ahd	P	154	219	3.4e-34	0.19	1.00		DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 1AHD 3 REPLACED BY SER (C39S) COMPLEX WITH DNA (NMR, 1AHD 4 16 STRUCTURES) 1AHD 5	
1044	1au7	A	145	213	3.8e-26	-0.39	0.65		PIT-1; CHAIN: A, B; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) GHF-1; COMPLEX (DNA-BINDING PROTEIN/DNA), PITUITARY, CPHD, 2 POU DOMAIN, TRANSCRIPTION FACTOR
1044	1b72	A	158	215	1.7e-27	0.20	1.00		HOMEODOMAIN PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA CHAIN: D; DNA CHAIN: E;	PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA
1044	1b8i	A	158	212	5.1e-29	0.33	1.00		ULTRABITHORAX HOMEOTIC PROTEIN IV; CHAIN: A; HOMEODOMAIN PROTEIN	TRANSCRIPTION/DNA ULTRABITHORAX; PBX PROTEIN; DNA BINDING, HOMEODOMAIN,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									EXTRADENTICLE; CHAIN: B; DNA (5'- CHAIN: C; DNA (5'- CHAIN: D;	HOMEOTIC PROTEINS, DEVELOPMENT, 2 SPECIFICITY
1044	1fjl	A	153	213	7.6e-26	0.16	1.00		PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION
1044	1fjl	B	155	211	1.9e-23	0.09	1.00		PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION
1044	1ftt		155	216	1.9e-23	0.03	0.96		THYROID TRANSCRIPTION FACTOR 1 HOMEODOMAIN; 1FTT 6 CHAIN: NULL; 1FTT 7	DNA BINDING PROTEIN TTF-1 HD; 1FTT 8 DNA BINDING PROTEIN, HOMEODOMAIN, TRANSCRIPTION FACTOR 1FTT 19
1044	1ftz		153	212	5.1e-29	0.16	0.99		DNA-BINDING FUSHI TARAZU PROTEIN (HOMEODOMAIN) (NMR, 20 STRUCTURES) 1FTZ 3	
1044	1nk2	P	146	223	6.8e-20			50.85	HOMEODOMAIN PROTEIN VND; CHAIN: P; DNA; CHAIN: A, B;	COMPLEX (HOMEODOMAIN/DNA) VND/NK-2 HOMEODOMAIN, VENTRAL NERVOUS SYSTEM HOMEODOMAIN, HOMEODOMAIN, DNA-BINDING PROTEIN, EMBRYONIC 2 DEVELOPMENT, COMPLEX (HOMEODOMAIN/DNA)
1044	1nk3	P	153	215	1.9e-25	0.26	1.00		HOMEODOMAIN PROTEIN VND; CHAIN: P; DNA; CHAIN: A, B;	COMPLEX (HOMEODOMAIN/DNA) VND/NK-2 HOMEODOMAIN, VENTRAL NERVOUS SYSTEM HOMEODOMAIN, HOMEODOMAIN, DNA-BINDING PROTEIN, EMBRYONIC 2 DEVELOPMENT, COMPLEX (HOMEODOMAIN/DNA) HELIX
1044	1san		160	219	8.5e-32	0.30	0.99		DNA-BINDING PROTEIN	

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 ISAN 3 REPLACED BY SER AND RESIDUES 1-6 DELETED (C39S,DEL 1-6) ISAN 4 (NMR, 20 STRUCTURES) ISAN 5	
1046	1a4y	A	41	214	0.0095	0.27	0.46		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS
1048	1cke	A	6	187	6.8e-22	-0.08	0.40		CYTIDINE MONOPHOSPHATE KINASE; CHAIN: A;	TRANSFERASE CK, MSSA; NUCLEOTIDE MONOPHOSPHATE KINASE,, TRANSFERASE
1048	1d6j	A	3	187	3.4e-23	0.08	0.33		ADENOSINE-5'PHOSPHOSULFATE KINASE; CHAIN: A, B;	TRANSFERASE APS KINASE; APS KINASE, ADENYLYLSULFATE KINASE, SULFATE, NUCLEOTIDE 2 KINASE, TRANSFERASE
1048	1qf9	A	3	185	1.7e-21	0.34	0.99		URIDYLMONOPHOSPHATE/CYTIDYLMONOPHOSPHATE KINASE; CHAIN: A;	KINASE UMP/CMP KINASE; NUCLEOSIDE MONOPHOSPHATE KINASE, NMP KINASE, PHOSPHORYL 2 TRANSFER, TRANSITION STATE ANALOG COMPLEX, TRANSFERASE
1048	1shk	A	1	186	1.7e-20	-0.06	0.84		SHIKIMATE KINASE; CHAIN: A, B;	TRANSFERASE SHIKIMATE KINASE, PHOSPHORYL TRANSFER, ADP, SHIKIMATE 2 PATHWAY, P-LOOP PROTEIN, TRANSFERASE
1048	1ukz		6	185	1.4e-19	0.35	0.64		TRANSFERASE URIDYLATE KINASE (E.C.2.7.4.-)	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									COMPLEXED WITH ADP AND AMP 1UKZ 3	
1048	2cmk	A	6	187	1.7e-21	0.01	0.12		CYTIDINE MONOPHOSPHATE KINASE; CHAIN: A;	TRANSFERASE CK; NUCLEOTIDE MONOPHOSPHATE KINASE, TRANSFERASE
1048	3adk		3	184	8.5e-22	-0.02	0.22		TRANSFERASE(PHOSPHOTRANSFERASE) ADENYLATE KINASE (E.C.2.7.4.3) 3ADK 4	
1049	1axi	B	162	349	1.7e-10	0.18	0.48		GROWTH HORMONE; CHAIN: A; GROWTH HORMONE RECEPTOR; CHAIN: B;	COMPLEX (HORMONE/RECEPTOR) HGH; HGHBP; COMPLEX (HORMONE/RECEPTOR)
1049	1bih	A	2	338	6.8e-21	0.21	-0.14		HEMOLIN; CHAIN: A; B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1049	1bj8		253	350	1.9e-14	0.35	0.42		GP130; CHAIN: NULL;	RECEPTOR RECEPTOR, SIGNAL TRANSDUCER OF IL-6 TYPE CYTOKINES, THIRD 2 N-TERMINAL DOMAIN, TRANSMEMBRANE, GLYCOPROTEIN
1049	1bj8		360	461	3.8e-09	0.07	0.33		GP130; CHAIN: NULL;	RECEPTOR RECEPTOR, SIGNAL TRANSDUCER OF IL-6 TYPE CYTOKINES, THIRD 2 N-TERMINAL DOMAIN, TRANSMEMBRANE, GLYCOPROTEIN
1049	1bj8		477	568	8.5e-12	0.27	0.01		GP130; CHAIN: NULL;	RECEPTOR RECEPTOR, SIGNAL TRANSDUCER OF IL-6 TYPE CYTOKINES, THIRD 2 N-TERMINAL DOMAIN, TRANSMEMBRANE, GLYCOPROTEIN
1049	1bj8		573	674	5.7e-19	0.25	0.35		GP130; CHAIN: NULL;	RECEPTOR RECEPTOR, SIGNAL TRANSDUCER OF IL-6 TYPE CYTOKINES, THIRD 2 N-TERMINAL DOMAIN, TRANSMEMBRANE,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1049	1bp3	B	158	354	1.2e-21	0.14	0.05		GROWTH HORMONE; CHAIN: A; PROLACTIN RECEPTOR; CHAIN: B;	GLYCOPROTEIN
1049	1bpv		159	259	3.8e-15	0.12	0.77		TITIN; CHAIN: NULL;	HORMONE/GROWTH FACTOR HORMONE, RECEPTOR, HORMONE/GROWTH FACTOR
1049	1bpv		257	351	3.8e-12	0.59	0.30		TITIN; CHAIN: NULL;	CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III
1049	1bpv		479	572	5.1e-11	-0.02	0.25		TITIN; CHAIN: NULL;	CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III
1049	1bpv		479	578	9.5e-14	0.09	0.15		TITIN; CHAIN: NULL;	CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III
1049	1bpv		577	675	3.8e-17	0.28	0.55		TITIN; CHAIN: NULL;	CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III
1049	1bqu	A	158	363	8.5e-19	0.02	-0.09		GPI30; CHAIN: A, B;	SIGNALING PROTEIN CYTOKINE RECEPTOR, GLYCOPROTEIN 130, GPI30, INTERLEUKINE 6 2 RECEPTOR BETA SUBUNIT, SIGNALING PROTEIN
1049	1bqu	A	159	347	1.9e-20	-0.07	0.21		GPI30; CHAIN: A, B;	SIGNALING PROTEIN CYTOKINE RECEPTOR, GLYCOPROTEIN 130, GPI30, INTERLEUKINE 6 2 RECEPTOR BETA SUBUNIT, SIGNALING PROTEIN
1049	1bqu	A	256	479	3.8e-12	0.25	0.03		GPI30; CHAIN: A, B;	SIGNALING PROTEIN CYTOKINE RECEPTOR, GLYCOPROTEIN 130, GPI30, INTERLEUKINE 6 2 RECEPTOR BETA SUBUNIT, SIGNALING PROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1049	1bqu	A	358	581	1.7e-14	-0.05	0.10		GP130; CHAIN: A, B;	SIGNALING PROTEIN CYTOKINE RECEPTOR, GLYCOPROTEIN 130, GP130, INTERLEUKINE 6 2 RECEPTOR BETA SUBUNIT, SIGNALING PROTEIN
1049	1bqu	A	479	681	6.8e-23	0.04	0.09		GP130; CHAIN: A, B;	SIGNALING PROTEIN CYTOKINE RECEPTOR, GLYCOPROTEIN 130, GP130, INTERLEUKINE 6 2 RECEPTOR BETA SUBUNIT, SIGNALING PROTEIN
1049	1c8p	A	256	352	3.8e-13	0.36	0.35		CYTOKINE RECEPTOR COMMON BETA CHAIN; CHAIN: A;	MEMBRANE PROTEIN BETA SANDWICH, CYTOKINE RECEPTOR, FN3 DOMAIN
1049	1c8p	A	359	457	7.6e-09	0.28	-0.12		CYTOKINE RECEPTOR COMMON BETA CHAIN; CHAIN: A;	MEMBRANE PROTEIN BETA SANDWICH, CYTOKINE RECEPTOR, FN3 DOMAIN
1049	1cd9	B	159	356	9.5e-27	0.17	0.24		GRANULOCYTE COLONY-STIMULATING FACTOR; CHAIN: A, C; G-CSF RECEPTOR; CHAIN: B, D;	CYTOKINE G-CSF; G-CSF-R; CLASS I CYTOKINE, HEMATOPOIETIC RECEPTOR, SIGNAL TRANSDUCTION
1049	1cd9	B	360	564	7.6e-16	0.14	0.06		GRANULOCYTE COLONY-STIMULATING FACTOR; CHAIN: A, C; G-CSF RECEPTOR; CHAIN: B, D;	CYTOKINE G-CSF; G-CSF-R; CLASS I CYTOKINE, HEMATOPOIETIC RECEPTOR, SIGNAL TRANSDUCTION
1049	1cfb		156	350	1.1e-34	-0.07	0.55		NEURAL ADHESION MOLECULE DROSOPHILA NEUROGLIAN (CHYMOTRYPTIC FRAGMENT CONTAINING THE ICFB 3 TWO AMINO PROXIMAL FIBRONECTIN TYPE III REPEATS ICFB 4 (RESIDUES 610 - 814) ICFB 5	
1049	1cfb		255	456	1.9e-23	0.20	0.90		NEURAL ADHESION	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									MOLECULE DROSOPHILA NEUROGLIAN (CHYMOTRYPTIC FRAGMENT CONTAINING THE 1CFB 3 TWO AMINO PROXIMAL FIBRONECTIN TYPE III REPEATS 1CFB 4 (RESIDUES 610 - 814)) 1CFB 5	
1049	1cfb		475	675	3.8e-31	0.17	0.42		NEURAL ADHESION MOLECULE DROSOPHILA NEUROGLIAN (CHYMOTRYPTIC FRAGMENT CONTAINING THE 1CFB 3 TWO AMINO PROXIMAL FIBRONECTIN TYPE III REPEATS 1CFB 4 (RESIDUES 610 - 814)) 1CFB 5	
1049	1cfb		479	670	1e-18	0.35	0.06		NEURAL ADHESION MOLECULE DROSOPHILA NEUROGLIAN (CHYMOTRYPTIC FRAGMENT CONTAINING THE 1CFB 3 TWO AMINO PROXIMAL FIBRONECTIN TYPE III REPEATS 1CFB 4 (RESIDUES 610 - 814)) 1CFB 5	
1049	1cs6	A	272	671	6.8e-23	0.00	-0.20		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1049	1cs6	A	2	349	1.7e-35	0.15	-0.08		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1049	1cs6	A	350	750	3.4e-15	0.12	-0.17		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1049	1cs6	A	67	464	6.8e-30	-0.08	0.10		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Coumpound	PDB annotation
1049	1cto		157	247	7.6e-13	-0.16	0.04		GRANULOCYTE COLONY-STIMULATING FACTOR RECEPTOR; CHAIN: NULL;	BINDING PROTEIN BINDING PROTEIN, CYTOKINE RECEPTOR
1049	1cto		259	350	3.8e-13	0.12	0.09		GRANULOCYTE COLONY-STIMULATING FACTOR RECEPTOR; CHAIN: NULL;	BINDING PROTEIN BINDING PROTEIN, CYTOKINE RECEPTOR
1049	1cto		479	585	7.6e-10	0.47	-0.09		GRANULOCYTE COLONY-STIMULATING FACTOR RECEPTOR; CHAIN: NULL;	BINDING PROTEIN BINDING PROTEIN, CYTOKINE RECEPTOR
1049	1cvs	C	74	250	6.8e-31	0.25	0.42		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1049	1cvs	D	2	135	1.5e-15	0.02	-0.15		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1049	1cvs	D	61	153	5.7e-20	-0.01	0.19		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1049	1cvs	D	74	250	1.7e-28	-0.03	0.51		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1049	1eer	B	474	555	1.5e-07	0.08	0.13		ERYTHROPOIETIN; CHAIN: A;	COMPLEX (CYTOKINE/RECEPTOR)

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									ERYTHROPOIETIN RECEPTOR; CHAIN: B, C;	EPOBP; ERYTHROPOIETIN, ERYTHROPOIETIN RECEPTOR, SIGNAL 2 TRANSDUCTION, HEMATOPOIETIC CYTOKINE, CYTOKINE RECEPTOR 3 CLASS 1, COMPLEX (CYTOKINE/RECEPTOR)
1049	1epf	A	67	222	3.8e-14	0.02	0.27		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1049	1epf	A	71	234	6.8e-13	0.13	0.07		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1049	1ev2	E	74	250	1.7e-26	-0.02	0.65		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE 1- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1049	1ev2	G	74	254	3.4e-30	-0.14	0.12		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE 1- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1049	1evt	C	64	213	5.7e-20	-0.08	0.58		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF1; FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE 1- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1049	1evt	C	74	250	1.7e-26	0.05	0.63		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF1; FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE 1-

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									C, D;	SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1049	1f6f	B	160	354	3.4e-24	0.28	0.51		PLACENTAL LACTOGEN; CHAIN: A; PROLACTIN RECEPTOR; CHAIN: B, C;	HORMONE/GROWTH FACTOR/HORMONE RECEPTOR 4-HELICAL BUNDLE, ALPHA HELICAL BUNDLE, TERNARY COMPLEX, FN 2 III DOMAINS, BETA SHEET DOMAINS, CYTOKINE-RECEPTOR COMPLEX
1049	1f6f	B	70	253	1.7e-16	-0.23	0.03		PLACENTAL LACTOGEN; CHAIN: A; PROLACTIN RECEPTOR; CHAIN: B, C;	HORMONE/GROWTH FACTOR/HORMONE RECEPTOR 4-HELICAL BUNDLE, ALPHA HELICAL BUNDLE, TERNARY COMPLEX, FN 2 III DOMAINS, BETA SHEET DOMAINS, CYTOKINE-RECEPTOR COMPLEX
1049	1f6f	C	192	352	7.6e-10	-0.11	0.71		PLACENTAL LACTOGEN; CHAIN: A; PROLACTIN RECEPTOR; CHAIN: B, C;	HORMONE/GROWTH FACTOR/HORMONE RECEPTOR 4-HELICAL BUNDLE, ALPHA HELICAL BUNDLE, TERNARY COMPLEX, FN 2 III DOMAINS, BETA SHEET DOMAINS, CYTOKINE-RECEPTOR COMPLEX
1049	1fhg	A	475	572	5.1e-08	0.18	-0.20		TELOKIN; CHAIN: A	CONTRACTILE PROTEIN IMMUNOGLOBULIN FOLD, BETA BARREL
1049	1fha		486	565	1.7e-13	0.23	0.16		CELL ADHESION PROTEIN FIBRONECTIN CELL-ADHESION MODULE TYPE III-10 IFNA 3	
1049	1fha		779	866	6.8e-09	0.38	-0.20		CELL ADHESION PROTEIN FIBRONECTIN CELL-ADHESION MODULE TYPE III-10 IFNA 3	

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1049	1fnf		158	565	5.1e-36	0.25	0.98		FIBRONECTIN; 1FNF 6 CHAIN: NULL; 1FNF 7	CELL ADHESION PROTEIN RGD, EXTRACELLULAR MATRIX 1FNF 18
1049	1fnf		159	575	5.1e-36			166.16	FIBRONECTIN; 1FNF 6 CHAIN: NULL; 1FNF 7	CELL ADHESION PROTEIN RGD, EXTRACELLULAR MATRIX 1FNF 18
1049	1fnf		479	866	3.4e-33	0.29	0.23		FIBRONECTIN; 1FNF 6 CHAIN: NULL; 1FNF 7	CELL ADHESION PROTEIN RGD, EXTRACELLULAR MATRIX 1FNF 18
1049	1fnf		68	459	1.7e-26	0.24	0.76		FIBRONECTIN; 1FNF 6 CHAIN: NULL; 1FNF 7	CELL ADHESION PROTEIN RGD, EXTRACELLULAR MATRIX 1FNF 18
1049	1fnf		772	977	3.4e-12	0.08	-0.20		FIBRONECTIN; 1FNF 6 CHAIN: NULL; 1FNF 7	CELL ADHESION PROTEIN RGD, EXTRACELLULAR MATRIX 1FNF 18
1049	1fnh	A	272	564	1.7e-20	0.22	0.55		FIBRONECTIN; CHAIN: A;	HEPARIN AND INTEGRIN BINDING
1049	1fnh	A	361	664	3.4e-27	0.26	0.07		FIBRONECTIN; CHAIN: A;	HEPARIN AND INTEGRIN BINDING
1049	1fnh	A	482	751	3.4e-23	0.12	-0.07		FIBRONECTIN; CHAIN: A;	HEPARIN AND INTEGRIN BINDING
1049	1fnh	A	580	855	8.5e-25	0.01	-0.19		FIBRONECTIN; CHAIN: A;	HEPARIN AND INTEGRIN BINDING
1049	1fnh	A	70	333	1.4e-18	0.29	0.98		FIBRONECTIN; CHAIN: A;	HEPARIN AND INTEGRIN BINDING
1049	1fnh	A	774	977	3.4e-20	0.05	-0.20		FIBRONECTIN; CHAIN: A;	HEPARIN AND INTEGRIN BINDING
1049	1mfn		157	343	1.1e-27	0.21	1.00		FIBRONECTIN; CHAIN: NULL;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2
1049	1mfn		162	343	3.4e-14	0.03	1.00		FIBRONECTIN; CHAIN: NULL;	HEPARIN-BINDING, GLYCOPROTEIN
1049	1mfn		259	456	1.1e-20	-0.04	0.49		FIBRONECTIN; CHAIN: NULL;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Coumpound	PDB annotation
										EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN
1049	1mfn		272	459	6.8e-11	0.13	0.45		FIBRONECTIN; CHAIN: NULL;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN
1049	1mfn		360	565	3.4e-20	0.05	0.13		FIBRONECTIN; CHAIN: NULL;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN
1049	1mfn		482	665	1.9e-27	0.24	0.17		FIBRONECTIN; CHAIN: NULL;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN
1049	1mfn		482	665	6.8e-25	0.20	-0.05		FIBRONECTIN; CHAIN: NULL;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN
1049	1nct		64	152	9.5e-23	0.16	1.00		TTTN; CHAIN: NULL;	MUSCLE PROTEIN CONNECTIN, NEXTM5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN
1049	1qg3	A	160	352	1.2e-15	0.19	0.99		INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;	STRUCTURAL PROTEIN INTEGRIN, HEMIDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2 PROTEIN

SEQ ID No.	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1049	1qg3	A	361	569	3.4e-19	0.11	0.59		INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;	STRUCTURAL PROTEIN INTEGRIN, HEMIDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2 PROTEIN
1049	1qg3	A	479	677	5.1e-26			103.51	INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;	STRUCTURAL PROTEIN INTEGRIN, HEMIDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2 PROTEIN
1049	1qg3	A	481	663	5.1e-26	0.23	0.43		INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;	STRUCTURAL PROTEIN INTEGRIN, HEMIDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2 PROTEIN
1049	1qg3	A	68	248	3.4e-17	0.29	0.66		INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;	STRUCTURAL PROTEIN INTEGRIN, HEMIDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2 PROTEIN
1049	1qr4	A	360	564	6.8e-12	0.24	0.43		TENASCIN; CHAIN: A, B;	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-III, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN
1049	1qr4	A	711	862	3.4e-08	0.09	-0.20		TENASCIN; CHAIN: A, B;	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-III, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN
1049	1qr4	A	776	971	3.4e-11	0.08	-0.20		TENASCIN; CHAIN: A, B;	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-III, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN
1049	1tit		65	150	1.1e-19	0.70	0.15		TITIN, I27; CHAIN: NULL;	IMMUNOGLOBULIN-LIKE DOMAIN CONNECTIN I27, TITIN IG REPEAT 27; MUSCLE PROTEIN,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1049	1tnm		67	152	1.9e-22	0.39	0.84		MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) 1TNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) 1TNM 4 1TNM 58	IMMUNOGLOBULIN-LIKE DOMAIN
1049	1ttf		776	866	1.7e-09	0.39	-0.20		GLYCOPROTEIN FIBRONECTIN (TENTH TYPE III MODULE) (NMR, 36 STRUCTURES) 1TTF 3	
1049	1wit		65	152	1.9e-22	0.66	-0.09		TWITCHIN 18TH IGSF MODULE; CHAIN: NULL;	MUSCLE PROTEIN IMMUNOGLOBULIN SUPERFAMILY, I SET, MUSCLE PROTEIN
1049	1wwc	A	64	163	1.1e-21	0.18	0.59		NT-3 GROWTH FACTOR RECEPTOR TRKC; CHAIN: A;	TRANSFERASE TRK RECEPTOR, RECEPTOR TYROSINE KINASE, 3D-DOMAIN SWAPPING, 2 TRANSFERASE
1049	2fcb	A	60	251	9.5e-13	-0.00	0.01		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
1049	2fnb	A	154	250	1.5e-14	0.55	0.68		FIBRONECTIN; CHAIN: A;	PROTEIN BINDING ED-B, FIBRONECTIN, TYPEIII DOMAIN, ANGIOGENESIS, PROTEIN 2 BINDING
1049	2fnb	A	255	345	9.5e-14	0.76	0.16		FIBRONECTIN; CHAIN: A;	PROTEIN BINDING ED-B, FIBRONECTIN, TYPEIII DOMAIN, ANGIOGENESIS, PROTEIN 2 BINDING
1049	2fnb	A	359	465	9.5e-10	0.02	0.10		FIBRONECTIN; CHAIN: A;	PROTEIN BINDING ED-B, FIBRONECTIN, TYPEIII DOMAIN, ANGIOGENESIS, PROTEIN 2 BINDING
1049	2fnb	A	475	570	1.9e-13	-0.12	0.04		FIBRONECTIN; CHAIN: A;	PROTEIN BINDING ED-B, FIBRONECTIN, TYPEIII DOMAIN, ANGIOGENESIS, PROTEIN 2 BINDING

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1049	2fmb	A	574	670	1.5e-16	0.10	0.28		FIBRONECTIN; CHAIN: A;	PROTEIN BINDING ED-B, FIBRONECTIN, TYPEIII DOMAIN, ANGIOGENESIS, PROTEIN 2 BINDING
1049	3hhr	B	162	349	1e-10	0.16	0.13		HORMONE/RECEPTOR HUMAN GROWTH HORMONE COMPLEXED WITH ITS RECEPTOR 3HHR 3 (EXTRACELLULAR DOMAIN) 3HHR 4	
1049	3hhr	B	162	351	3.8e-27	0.24	0.03		HORMONE/RECEPTOR HUMAN GROWTH HORMONE COMPLEXED WITH ITS RECEPTOR 3HHR 3 (EXTRACELLULAR DOMAIN) 3HHR 4	
1049	3ncm	A	65	154	3.8e-23	0.45	0.46		NEURAL CELL ADHESION MOLECULE, LARGE ISOFORM; CHAIN: A;	CELL ADHESION PROTEIN NCAM MODULE 2; CELL ADHESION, GLYCOPROTEIN, HEPARIN-BINDING, GPI-ANCHOR, 2 NEURAL ADHESION MOLECULE, IMMUNOGLOBULIN FOLD, HOMOPHILIC 3 BINDING, CELL ADHESION PROTEIN
1050	1bth	A	20	157	3.4e-29	0.09	-0.06		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1050	1cs6	A	4	158	3.4e-34	0.02	0.07		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1050	1evs	C	3	157	3.4e-41	0.12	-0.05		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN:	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1050	1evs	D	3	157	6.8e-42	0.22	0.33		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1050	1epf	A	2	143	6.8e-22	-0.00	0.64		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1050	1ev2	E	3	157	1.7e-36	0.08	0.05		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1050	1ev2	E	90	162	8.5e-14	0.21	-0.05		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1050	1evt	C	3	157	1e-41	0.08	0.54		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF1; FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1050	1f2q	A	2	162	1.7e-23	0.19	0.54		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A;	IMMUNE SYSTEM FC-EPSILON RI-ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN
1050	1f0g	A	2	159	8.5e-24	-0.02	0.90		FC RECEPTOR	IMMUNE SYSTEM, MEMBRANE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									FC(GAMMA)RIIA; CHAIN: A;	PROTEIN CD32; FC RECEPTOR, IMMUNOGLOBULIN, LEUKOCYTE, CD32
1050	1fhg	A	1	75	1.2e-12	-0.10	0.63		TELOKIN; CHAIN: A	CONTRACTILE PROTEIN IMMUNOGLOBULIN FOLD, BETA BARREL
1050	1fhg	A	76	157	3.4e-17	0.37	-0.14		TELOKIN; CHAIN: A	CONTRACTILE PROTEIN IMMUNOGLOBULIN FOLD, BETA BARREL
1050	1fhl	A	2	147	1.9e-20	0.00	0.31		LOW AFFINITY IMMUNOGLOBULIN GAMMA FC REGION CHAIN: A;	IMMUNE SYSTEM RECEPTOR BETA SANDWICH, IMMUNOGLOBULIN-LIKE, RECEPTOR
1050	1nct		2	75	1.2e-12	0.07	0.87		TITIN; CHAIN: NULL;	MUSCLE PROTEIN CONNECTIN, NEXTM5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN
1050	1nct		80	158	1.7e-16	0.20	-0.09		TITIN; CHAIN: NULL;	MUSCLE PROTEIN CONNECTIN, NEXTM5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN
1050	1tnm		2	75	1.2e-12	0.43	0.54		MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) 1TNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) 1TNM 4 1TNM 58	
1050	1tnm		80	158	1.7e-16	0.07	-0.12		MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) 1TNM 3 (NMR, MINIMIZED	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									AVERAGE STRUCTURE) 1TNM 4 1TNM 58	
1050	2dli	A	2	146	1.9e-19	-0.26	0.09		MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	IMMUNE SYSTEM P58 NATURAL KILLER CELL RECEPTOR; KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN
1050	2fcb	A	2	160	6.8e-25	0.14	0.69		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
1051	1aln	A	26	115	3.4e-43	-0.16	0.30		B*3501; CHAIN: A, B; PEPTIDE VPLRPMY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1051	1agd	A	26	115	3.4e-43	0.06	0.25		B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1051	1duz	A	26	115	1.7e-42	0.18	0.22		HLA-A*0201; CHAIN: A, D; BETA-2 MICROGLOBULIN; CHAIN: B, E; HTLV-1 OCTAMERIC TAX PEPTIDE; CHAIN: C, F;	IMMUNE SYSTEM IMMUNOGLOBULIN FOLD
1051	1efx	A	26	115	5.1e-43	0.24	0.28		HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D, E;	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1051	1hoc	A	26	116	1.4e-42	0.34	0.69		HISTOCOMPATIBILITY ANTIGEN MURINE CLASS I	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									MAJOR HISTOCOMPATIBILITY COMPLEX CONSISTING 1HOC 3 OF H-2D==B==, B2-MICROGLOBULIN, AND A 9-RESIDUE PEPTIDE 1HOC 4	
1051	1hsb	A	26	115	8.5e-44	0.08	0.40		HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE 1HSB 3 ANTIGEN) 1HSB 4	
1051	1mhe	A	26	115	8.5e-43	0.13	0.25		HLA CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-E; CHAIN: A, C; BETA-2-MICROGLOBULIN; CHAIN: B, D; PEPTIDE (VMAPRTVLL); CHAIN: P, Q;	MAJOR HISTOCOMPATIBILITY COMPLEX MHC NONCLASSICAL CHAIN, MHC-E, HLA-E, MHC CLASS HLA-E, HLA E, MAJOR HISTOCOMPATIBILITY COMPLEX, MHC, HLA, 2 BETA 2 MICROGLOBULIN, PEPTIDE, LEADER PEPTIDE, 3 NON-CLASSICAL MHC, CLASS IB MHC
1051	1osz	A	26	115	1.2e-43	0.13	0.37		MHC CLASS I H-2KB HEAVY CHAIN; CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; VESICULAR STOMATITIS VIRUS NUCLEOPROTEIN; CHAIN: C;	COMPLEX (MHC I/PEPTIDE) VSV-8; MHC/PEPTIDE COMPLEX, TRANSMEMBRANE PROTEIN, THYMIC 2 SELECTION, COMPLEX (MHC I/PEPTIDE)
1051	1qo3	A	26	115	3.4e-42	0.10	0.39		MHC CLASS I H-2DD HEAVY CHAIN; CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; HIV ENVELOPE GLYCOPROTEIN 120 PEPTIDE; CHAIN: P; LY49A; CHAIN: C, D;	COMPLEX (NK RECEPTOR/MHC CLASS I) H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, B2M; NK-CELL SURFACE GLYCOPROTEIN YE1/48, NK CELL, INHIBITORY RECEPTOR, MHC-I, C-TYPE LECTIN-LIKE, 2 HISTOCOMPATIBILITY, B2M, LY49,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1051	1tmc	A	26	115	8.5e-44	0.43	0.52		HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-A*W68 ITMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) ITMC 4	LY-49
1068	1mey	C	568	650	3.4e-49			100.26	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1068	1tf6	A	596	762	8.5e-38			108.39	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1068	2gli	A	327	466	3.4e-34			89.55	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1070	1a25	A	160	291	5.1e-37			68.22	PROTEIN KINASE C (BETA); CHAIN: A, B;	CALCIUM-BINDING PROTEIN CALB; CALCIUM++/PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM-BINDING PROTEIN
1070	1rsy		154	283	3.4e-44			97.42	CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2	

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									DOMAIN) (CALB) IRSY 3	
1075	1got	B	1	322	5.1e-89			116.65	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
1078	1got	B	3	345	5.1e-81			104.69	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
1084	1mey	C	330	412	1.4e-48			107.26	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1084	1tf6	A	750	913	1e-37			114.17	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1084	2gli	A	302	441	1.4e-33			103.60	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI;

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										GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1090	1evh	A	9	122	3.4e-50			82.80	MENA EVH1 DOMAIN; CHAIN: A; PEPTIDE ACTA; CHAIN: B;	CONTRACTILE PROTEIN WHI DOMAIN; MOLECULAR RECOGNITION, ACTIN DYNAMICS, CONTRACTILE PROTEIN
1090	1qc6	A	9	121	1.7e-44			62.71	EVH1 DOMAIN FROM ENA/ASP-LIKE PROTEIN; CHAIN: A, B; PHE-GLU-PHE-PRO-PRO-PRO-THR-ASP-GLU-GLU; CHAIN: C, D;	CELL MOTILITY AN INCOMPLETE SEVEN STRANDED ANTI-PARALLEL BETA BARREL 2 CLOSED BY AN ALPHA HELIX, EVH1 DOMAIN, ACTIN-BASED CELL 3 MOTILITY, INTERACTION MODULE
1095	1alh	A	391	473	1.7e-26			84.85	QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1095	1mey	C	418	500	1.4e-45			110.38	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1095	1tf6	A	362	530	3.4e-34			120.65	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1095	1ubd	C	336	444	3.4e-33			98.51	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1095	2gli	A	334	473	6.8e-34			105.76	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX REGULATION/DNA)
1101	1edh	A	62	266	5.1e-48			122.19	E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
1101	1ncj	A	61	265	6.8e-50			122.52	N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
1105	1aj4		72	237	8.5e-36			73.76	TROPONIN C; CHAIN: NULL;	MUSCLE PROTEIN CTNC; CARDIAC, MUSCLE PROTEIN, REGULATORY, CALCIUM BINDING
1105	1au1	B	74	249	1.7e-39			92.24	SERINE/THREONINE PHOSPHATASE 2B; CHAIN: A, B;	HYDROLASE CALCINEURIN; HYDROLASE, PHOSPHATASE, IMMUNOSUPPRESSION
1105	1bjf	A	65	245	1.7e-49			184.52	NEUROCALCIN DELTA; CHAIN: A, B;	CALCIUM-BINDING CALCIUM-BINDING, MYRISTOYLATION, NEURONAL SPECIFIC GUANYLATE 2 CYCLASE ACTIVATOR
1105	1cdm	A	82	234	1.4e-55			57.84	CALCIUM-BINDING PROTEIN CALMODULIN COMPLEXED WITH CALMODULIN-BINDING DOMAIN OF 1CDM 3 CALMODULIN-DEPENDENT PROTEIN KINASE II 1CDM 4	
1105	1cll		82	235	3.4e-60			67.88	CALCIUM-BINDING PROTEIN	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CALMODULIN (VERTEBRATE) ICLL 3	
1105	liku		62	245	3.4e-39			160.57	RECOVERIN; CHAIN: NULL;	CALCIUM-BINDING PROTEIN CALCIUM-MYRISTOYL SWITCH, CALCIUM-BINDING PROTEIN
1105	lrec		68	250	1.7e-34			143.82	CALCIUM-BINDING PROTEIN RECOVERIN (CALCIUM SENSOR IN VISION) IREC 3	
1105	ltcf		70	235	1.5e-39			73.38	TROPONIN C; CHAIN: NULL;	CALCIUM-REGULATED MUSCLE CONTRACTION MUSCLE CONTRACTION, CALCIUM- BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION REGULATORY DOMAIN, CALCIUM- REGULATED 3 MUSCLE CONTRACTION
1105	ltmx		67	233	1e-38			69.96	TROPONIN C; ITNX 4 CHAIN: NULL; ITNX 5	CALCIUM-BINDING PROTEIN EF- HAND ITNX 14
1105	ltop		63	237	8.5e-40			73.36	CONTRACTILE SYSTEM PROTEIN TROPONIN C ITOP 3	
1105	lvnk	A	79	236	3.4e-59			68.28	CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
1105	2scp	A	34	205	3.4e-09			53.97	BINDING PROTEIN SARCOPLASMIC CALCIUM- BINDING PROTEIN 2SCP 3	
1114	lam4	D	51	216	6.8e-48			70.86	P50-RHOGAP; CHAIN: A, B, C; CDC42HS; CHAIN: D, E, F;	COMPLEX (GTPASE- ACTIVATING/GTP-BINDING) COMPLEX (GTPASE- ACTIVATING/GTP-BINDING), GTPASE ACTIVATION
1114	lbyu	A	45	231	8.5e-52			74.78	GTP-BINDING PROTEIN RAN;	TRANSPORT PROTEIN TC4; GTPASE,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Coumpound	PDB annotation
									CHAIN: A, B;	NUCLEAR TRANSPORT, TRANSPORT PROTEIN
1114	lbyu	B	41	231	1.7e-52			69.65	GTP-BINDING PROTEIN RAN; CHAIN: A, B;	TRANSPORT PROTEIN TC4; GTPASE, NUCLEAR TRANSPORT, TRANSPORT PROTEIN
1114	lcly	A	50	216	1.7e-63			67.97	RAS-RELATED PROTEIN RAP-1A; CHAIN: A; PROTO-ONKOGENE SERINE/THREONINE PROTEIN KINASE CHAIN: B;	SIGNALING PROTEIN GTP-BINDING PROTEINS, PROTEIN-PROTEIN COMPLEX, EFFECTORS
1114	lctq	A	50	217	1.7e-62			75.99	TRANSFORMING PROTEIN P21/H-RAS-1; CHAIN: A;	SIGNALING PROTEIN G PROTEIN, GTP HYDROLYSIS, KINETIC CRYSTALLOGRAPHY, 2 SIGNALING PROTEIN
1114	lczx	A	47	222	1.5e-54			82.44	HIS-TAGGED TRANSFORMING PROTEIN RHOA(0-181); CHAIN: A; PKN; CHAIN: B;	SIGNALING PROTEIN PROTEIN-PROTEIN COMPLEX, ANTIPARALLEL COILED-COIL
1114	lhur	A	37	218	5.1e-12			71.40	HUMAN ADP-RIBOSYLATION FACTOR 1; IHUR 5 CHAIN: A, B; IHUR 7	PROTEIN TRANSPORT GDP-BINDING, MEMBRANE TRAFFICKIN, NON-MYRISTOYLATED IHUR 16
1114	lbr	A	52	221	3.4e-51			86.05	RAN; CHAIN: A, C; IMPORTIN BETA SUBUNIT; CHAIN: B, D;	SMALL GTPASE KARYOPHERIN BETA, P95 SMALL GTPASE, NUCLEAR TRANSPORT RECEPTOR
1114	lkao		50	217	3.4e-60			79.99	RAP2A; CHAIN: NULL;	GTP-BINDING PROTEIN GTP-BINDING PROTEIN, SMALL G PROTEIN, RAP2, GDP, RAS
1114	lmh1		49	222	1.2e-54			77.42	RAC1; CHAIN: NULL;	GTP-BINDING GTP-BINDING, GTPASE, SMALL G-PROTEIN, RHO FAMILY, RAS SUPER 2 FAMILY
1114	lrrp	C	47	231	3.4e-51			89.47	RAN; CHAIN: A, C; NUCLEAR PORE COMPLEX PROTEIN NUP358; CHAIN: B, D;	COMPLEX (SMALL GTPASE/NUCLEAR PROTEIN) COMPLEX (SMALL GTPASE/NUCLEAR PROTEIN), SMALL GTPASE, 2 NUCLEAR

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1114	1tx4	B	51	216	1.4e-51			70.72	P50-RHOGAP; CHAIN: A; TRANSFORMING PROTEIN RHOA; CHAIN: B;	TRANSPORT COMPLEX(GTPASE ACTIVATN/PROTO-ONCOGENE) GTPASE-ACTIVATING PROTEIN RHOGAP; COMPLEX (GTPASE ACTIVATION/PROTO-ONCOGENE), GTPASE, 2 TRANSITION STATE, GAP COMPLEX (GTP- BINDING/EFFECTOR) RAS-RELATED PROTEIN RAB3A; COMPLEX (GTP- BINDING/EFFECTOR), G PROTEIN, EFFECTOR, RABCDR, 2 SYNAPTIC EXOCYTOSIS, RAB PROTEIN, RAB3A, RABPHILIN
1114	1zbd	A	49	226	1.7e-63			93.30	RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;	
1114	2ngr	A	50	230	3.4e-50			77.06	GTP BINDING PROTEIN (G25K); CHAIN: A; GTPASE ACTIVATING PROTEIN (RHG); CHAIN: B;	HYDROLASE CDC42/CDC42GAP; CDC42/CDC42GAP; TRANSITION STATE, G-PROTEIN, GAP, CDC42, ALF3, HYDROLASE
1114	3rab	A	47	221	6.8e-65			102.45	RAB3A; CHAIN: A;	HYDROLASE G PROTEIN, VESICULAR TRAFFICKING, GTP HYDROLYSIS, RAB 2 PROTEIN, NEUROTRANSMITTER RELEASE, HYDROLASE
1116	2bnh		2	324	1.7e-52			56.47	RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLTATION, LEUCINE-RICH REPEATS
1120	5pnt		2	140	1.4e-54			214.70	LOW MOLECULAR WEIGHT PHOSPHOTYROSYL PHOSPHATASE; CHAIN: NULL;	HYDROLASE ORTHOPHOSPHORIC MONOESTER PHOSPHOHYDROLASE; HYDROLASE, ACETYLTATION, TYROSINE PHOSPHATASE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1122	1av1	A	83	280	5.1e-05			51.65	APOLIPOPROTEIN A-I; CHAIN: A, B, C, D;	LIPID TRANSPORT APO A-I; LIPOPROTEIN, LIPID TRANSPORT, CHOLESTEROL METABOLISM, 2 ATHEROSCLEROSIS, HDL, LCAT-ACTIVATION
1127	1a0l	A	465	741	3.4e-76			100.75	BETA-TRYPTASE; CHAIN: A, B, C, D;	SERINE PROTEINASE TRYPSIN-LIKE SERINE PROTEINASE, TETRAMER, HEPARIN, ALLERGY, 2 ASTHMA
1127	1a5i	A	454	739	5.1e-67			106.52	PLASMINOGEN ACTIVATOR; CHAIN: A; GLU-GLY-ARG CHLOROMETHYL KETONE; CHAIN: I;	COMPLEX (SERINE PROTEINASE/INHIBITOR) (DELTA FEK) DSPAALPHA1; EGRCMK; SERINE PROTEASE, FIBRINOLYTIC ENZYMES, PLASMINOGEN 2 ACTIVATORS
1127	1aht	H	465	744	1.5e-73			91.53	ALPHA-THROMBIN; 1AHT 4 CHAIN: L, H; 1AHT 5 HIRUGEN; 1AHT 8 CHAIN: I; 1AHT 9	COMPLEX (SERINE PROTEINASE/INHIBITOR)
1127	1aut	C	464	739	5.1e-68			99.33	ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE, PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
1127	1ekb	B	468	739	1.7e-76			89.82	ENTEROPEPTIDASE; CHAIN: A; ENTEROPEPTIDASE; CHAIN: B; VAL-ASP-ASP-ASP-LYS PEPTIDE; CHAIN: C;	HYDROLASE/HYDROLASE INHIBITOR ENTEROKINASE, HEAVY CHAIN; ENTEROKINASE, LIGHT CHAIN; ENTEROPEPTIDASE, TRYPSINOGEN ACTIVATION, 2 HYDROLASE/HYDROLASE INHIBITOR

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1127	1etr	H	465	745	1.5e-71			92.09	HYDROLASE(SERINE PROTEINASE) EPSILON-THROMBIN (E.C.3.4.21.5) NON-COVALENT COMPLEX WITH IETR 3 MQPA IETR 4	
1127	1fxy	A	463	742	1.4e-76			89.40	COAGULATION FACTOR XA-TRYPSIN CHIMERA; CHAIN: A; D-PHE-PRO-ARG-CHLOROMETHYLKETONE (PPACK) WITH CHAIN: I; FACTOR XA; CHAIN: H, L; ANTICOAGULANT PEPTIDE; CHAIN: I;	COMPLEX (PROTEASE/INHIBITOR) TRYPSIN, COAGULATION FACTOR XA, CHIMERA, PROTEASE, PPACK, 2 CHLOROMETHYLKETONE, COMPLEX (PROTEASE/INHIBITOR)
1127	1kig	H	465	745	3.4e-70			98.96	FACTOR XA; CHAIN: H, L; ANTICOAGULANT PEPTIDE; CHAIN: I;	COMPLEX (PROTEASE/INHIBITOR) RTAP; GLYCOPROTEIN, SERINE PROTEASE, PLASMA, BLOOD COAGULATION, 2 COMPLEX (PROTEASE/INHIBITOR)
1127	1mkx	K	425	739	1.7e-72			93.49	ALPHA-THROMBIN; CHAIN: L; H; PRETHROMBIN-2; CHAIN: K;	COMPLEX (BLOOD COAGULATION/PROENZYME) COMPLEX (BLOOD COAGULATION/PROENZYME), THROMBIN, 2 PRETHROMBIN-2, PLASMA, SERINE PROTEASE
1127	1pyt	D	454	739	1.5e-75			95.69	PROCARBOXYPEPTIDASE A; CHAIN: A, B; PROPROTEINASE E; CHAIN: C; CHYMOTRYPSINOGEN C; CHAIN: D;	TERNARY COMPLEX (ZYMOGEN) TC, PCPA-TC; TERNARY COMPLEX (ZYMOGEN), SERINE PROTEINASE, C-TERMINAL 2 PEPTIDASE
1127	1rtf	B	467	740	1.7e-68			102.89	TWO CHAIN TISSUE PLASMINOGEN ACTIVATOR; CHAIN: A, B;	SERINE PROTEASE (TC)-T-PA; SERINE PROTEASE, FIBRINOLYTIC ENZYMES
1135	1mey	C	342	430	6.8e-47			71.69	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1135	1tf3	A	342	433	1.5e-21			67.88	TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	(ZINC FINGER/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
1135	1tf6	A	276	454	3.4e-41			105.09	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE II, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1135	1ubd	C	277	400	1.7e-30			80.44	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1135	2gli	A	277	431	1.4e-60			202.77	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1139	1mab	B	1	183	1.7e-46			64.40	F1-ATPASE ALPHA CHAIN; CHAIN: A; F1-ATPASE BETA CHAIN; CHAIN: B; F1-ATPASE GAMMA CHAIN; CHAIN: G;	HYDROLASE ATP SYNTHASE, FOF1-ATPASE, OXIDATIVE PHOSPHORYLATION, 2 MITOCHONDRIA, HYDROLASE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1140	1mab	B	51	264	6.8e-66			130.11	F1-ATPASE ALPHA CHAIN; CHAIN: A; F1-ATPASE BETA CHAIN; CHAIN: B; F1-ATPASE GAMMA CHAIN; CHAIN: G;	HYDROLASE ATP SYNTHASE, FOF1-ATPASE, OXIDATIVE PHOSPHORYLATION, 2 MITOCHONDRIA, HYDROLASE
1148	1crz	A	3	122	1.6e-09	0.19	0.17		TOLB PROTEIN; CHAIN: A;	TOXIN BINDING PROTEIN TWO DOMAINS: BETA PROPELLER AND ALPHA/BETA FOLD
1148	1erj	A	11	127	3.2e-29	0.70	0.94		TRANSCRIPTIONAL REPRESSOR TUPI; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
1148	1erj	A	3	79	3.2e-10	0.16	0.18		TRANSCRIPTIONAL REPRESSOR TUPI; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
1148	1got	B	6	122	8e-22	0.01	0.40		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
1149	1efl	A	43	326	1.4e-97	0.69	1.00		MOESIN; CHAIN: A, B; MOESIN; CHAIN: C, D;	MEMBRANE PROTEIN CRYSTAL STRUCTURE, MEMBRANE, FERM DOMAIN, TAIL DOMAIN
1153	1a06		36	339	0			329.67	CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE; CHAIN: NULL;	KINASE KINASE, SIGNAL TRANSDUCTION, CALCIUM/CALMODULIN
1153	1a06		6	334	0	0.64	1.00		CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE; CHAIN: NULL;	KINASE KINASE, SIGNAL TRANSDUCTION, CALCIUM/CALMODULIN

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1155	1cfe		51	203	1e-28			82.01	PATHOGENESIS-RELATED PROTEIN P14A; CHAIN: NULL;	PATHOGENESIS-RELATED PROTEIN PATHOGENESIS-RELATED LEAF PROTEIN 6, ETHYLENE PATHOGENESIS-RELATED PROTEIN, PR-1 PROTEINS, 2 PLANT DEFENSE
1155	1cfe		52	203	1e-28	0.47	1.00		PATHOGENESIS-RELATED PROTEIN P14A; CHAIN: NULL;	PATHOGENESIS-RELATED PROTEIN PATHOGENESIS-RELATED LEAF PROTEIN 6, ETHYLENE PATHOGENESIS-RELATED PROTEIN, PR-1 PROTEINS, 2 PLANT DEFENSE
1156	1ds6	A	1	96	1.2e-46	0.06	1.00		RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 2; CHAIN: A; RHO GDP-DISSOCIATION INHIBITOR 2; CHAIN: B;	SIGNALING PROTEIN P21-RAC2; RHO GDI 2, RHO-GDI BETA, LY-GDI; BETA SANDWHICH, PROTEIN- PROTEIN COMPLEX, G-DOMAIN, 2 IMMUNOGLOBULIN FOLD, WALKER FOLD, GTP-BINDING PROTEIN
1159	1qf9	A	23	239	1.5e-19	-0.03	0.62		URIDYLMONOPHOSPHATE/CYTIDYLMONOPHOSPHATE KINASE; CHAIN: A;	KINASE UMP/CMP KINASE; NUCLEOSIDE MONOPHOSPHATE KINASE, NMP KINASE, PHOSPHORYL 2 TRANSFER, TRANSITION STATE ANALOG COMPLEX, TRANSFERASE
1159	1qhf	A	249	424	5.1e-47	0.47	1.00		PHOSPHOGLYCERATE MUTASE; CHAIN: A, B;	TRANSFERASE TRANSFERASE (PHOSPHORYL)
1159	1qhf	A	250	449	5.1e-47			63.00	PHOSPHOGLYCERATE MUTASE; CHAIN: A, B;	TRANSFERASE TRANSFERASE (PHOSPHORYL)
1159	3adk		36	236	3.4e-26	-0.17	0.68		TRANSFERASE(PHOSPHOTRANSFERASE) ADENYLATE KINASE (E.C.2.7.4.3) 3ADK 4	

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1159	3pgm		249	441	1.7e-48	0.19	1.00		TRANSFERASE (PHOSPHORYL) PHOSPHOGLYCERATE MUTASE (E.C.2.7.5.3) DE- PHOSPHO ENZYME 3PGM 4	
1159	3pgm		249	441	1.7e-48			58.96	TRANSFERASE (PHOSPHORYL) PHOSPHOGLYCERATE MUTASE (E.C.2.7.5.3) DE- PHOSPHO ENZYME 3PGM 4	
1159	3tmk	A	34	237	1.2e-29	-0.13	0.19		THYMIDYLATE KINASE; CHAIN: A, B, C, D, E, F, G, H;	KINASE KINASE, PHOSPHOTRANSFERASE
1160	1mey	C	360	442	4.8e-51			100.83	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1160	1tf6	A	276	437	8e-38			108.88	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1160	1ubd	C	334	442	5.1e-53			86.63	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1160	2gli	A	304	443	3.2e-34			98.31	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										BINDING PROTEIN/DNA)
1163	1a06		43	340	3.2e-84			130.42	CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE; CHAIN: NULL;	KINASE KINASE, SIGNAL TRANSDUCTION, CALCIUM/CALMODULIN
1163	1a60		18	334	6.8e-54			108.45	PROTEIN KINASE CK2/ALPHA-SUBUNIT; CHAIN: NULL;	TRANSFERASE TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, CASEIN KINASE, 2 SER/THR KINASE
1163	1apm	E	18	353	0			168.88	TRANSFERASE(PHOSPHOTRANSFERASE) \$C-/AMP\$-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (\$C/APK\$) 1APM 3 (CATALYTIC SUBUNIT) ALPHA ISOENZYME MUTANT WITH SER 139 1APM 4 REPLACED BY ALA (S139A\$) COMPLEX WITH THE PEPTIDE 1APM 5 INHIBITOR PKI(5-24) AND THE DETERGENT MEGA-8 1APM 6	
1163	1aq1		50	348	4.8e-56			111.26	CYCLIN-DEPENDENT PROTEIN KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; PROTEIN KINASE, CELL CYCLE, PHOSPHORYLATION, STAUROSPORINE, 2 CELL DIVISION, MITOSIS, INHIBITION
1163	1b18	A	51	323	6.8e-56			93.00	CYCLIN-DEPENDENT KINASE 6; CHAIN: A, C; CYCLIN-DEPENDENT KINASE INHIBITOR; CHAIN: B, D;	COMPLEX (KINASE/INHIBITOR) CDK6; P19INK4D; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, COMPLEX (KINASE/INHIBITOR) HEADER HELIX
1163	1b1x	A	47	331	6.8e-62			113.75	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN:	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									B;	PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1163	1byg	A	44	300	1.3e-31			93.49	C-TERMINAL SRC KINASE; CHAIN: A;	TRANSFERASE CSK; PROTEIN KINASE, C-TERMINAL SRC KINASE, PHOSPHORYLATION, 2 STAUROSPORINE, TRANSFERASE
1163	1cmk	E	9	353	0			175.36	PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT 1CMK 3 (E.C.2.7.1.37) 1CMK 4	
1163	1ctp	E	15	343	0			168.10	TRANSFERASE(PHOSPHOTRANSFERASE) CAMP-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) 1CTP 3 (CATALYTIC SUBUNIT) 1CTP 4	
1163	1fgk	A	39	309	6.4e-31			106.44	FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE
1163	1fgk	B	36	304	1.3e-37			117.87	FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE
1163	1hcl		50	348	1e-66			128.78	HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1163	1ir3	A	38	323	3.2e-26			99.07	INSULIN RECEPTOR; CHAIN: A; PEPTIDE SUBSTRATE; CHAIN: B;	KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION COMPLEX (TRANSFERASE/SUBSTRATE) TYROSINE KINASE, SIGNAL TRANSDUCTION, PHOSPHOTRANSFERASE, 2 COMPLEX (KINASE/PEPTIDE SUBSTRATE/ATP ANALOG), ENZYME, 3 COMPLEX (TRANSFERASE/SUBSTRATE)
1163	1jnk		38	388	5.1e-64			104.42	C-JUN N-TERMINAL KINASE; CHAIN: NULL;	TRANSFERASE JNK3; TRANSFERASE, JNK3 MAP KINASE, SERINE/THREONINE PROTEIN 2 KINASE
1163	1kob	A	24	359	1e-90			159.16	TWITCHIN; CHAIN: A, B;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
1163	1p38		31	395	1.6e-50			109.88	MAP KINASE P38; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE; TRANSFERASE, MAP KINASE, SERINE/THREONINE-PROTEIN KINASE, 2 P38
1163	1phk		49	305	1.1e-83			156.26	PHOSPHORYLASE KINASE; CHAIN: NULL;	KINASE RABBIT MUSCLE PHOSPHORYLASE KINASE; GLYCOGEN METABOLISM, TRANSFERASE, SERINE/THREONINE-PROTEIN, 2 KINASE, ATP-BINDING, CALMODULIN-BINDING
1163	1pme		44	389	9.6e-46			104.21	ERK2; CHAIN: NULL;	TRANSFERASE MAP KINASE, SERINE/THREONINE PROTEIN KINASE, TRANSFERASE
1163	1tki	A	47	370	8e-57			131.84	TITIN; CHAIN: A, B;	SERINE KINASE SERINE KINASE,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1163	3erk		36	400	3.4e-69			116.38	EXTRACELLULAR REGULATED KINASE 2; CHAIN: NULL;	TITIN, MUSCLE, AUTONHIBITION TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE, MAP 2, ERK2; TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, MAP KINASE, 2 ERK2
1170	1bw m	A	17	247	1.6e-12			50.07	ALPHA-BETA T CELL RECEPTOR (TCR) (D10); CHAIN: A;	IMMUNE SYSTEM IMMUNOGLOBULIN, IMMUNORECEPTOR, IMMUNE SYSTEM
1170	1cdy		22	190	0.00034			50.90	T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: NULL;	T-CELL SURFACE GLYCOPROTEIN IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, T-CELL, 2 MHC, LIPOPROTEIN, T-CELL SURFACE GLYCOPROTEIN
1170	1f58	H	17	244	4.8e-21			51.50	IGG1 ANTIBODY 58.2 (LIGHT CHAIN); CHAIN: L; IGG1 ANTIBODY 58.2 (HEAVY CHAIN); CHAIN: H; EXTERIOR MEMBRANE GLYCOPROTEIN(GP120); CHAIN: P;	IMMUNE SYSTEM FAB 58.2; FAB 58.2; V3 LOOP; IMMUNOGLOBULIN, FAB, HIV-1, GP120, V3, IMMUNE SYSTEM
1170	1fig	H	17	239	8e-19			51.43	IMMUNOGLOBULIN IMMUNOGLOBULIN G1 (KAPPA LIGHT CHAIN) FAB' FRAGMENT IFIG 3	
1170	1qrm	D	14	219	6.4e-23			50.17	MHC CLASS I HLA-A; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE P6A; CHAIN: C; HMAN T-CELL RECEPTOR; CHAIN: D; HLA-A 0201; CHAIN: E;	IMMUNE SYSTEM HUMAN TCR/PEPTIDE/MHC COMPLEX, HLA-A2, HTLV-1, TAX, TCR, T 2 CELL RECEPTOR, IMMUNE SYSTEM

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1170	2gfb	A	15	240	1.6e-17			51.08	IMMUNOGLOBULIN IGG2A FAB FRAGMENT (CNJ206) 2GFB 3	
1170	2pcp	B	17	239	9.6e-21			51.13	IMMUNOGLOBULIN; CHAIN: A, B, C, D;	IMMUNOGLOBULIN IMMUNOGLOBULIN
1174	1a17		152	245	0.0017	-0.20	0.04		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
1180	1fib		195	418	1.7e-53			129.15	GAMMA-FIBRINOGEN CARBOXYL TERMINAL FRAGMENT; CHAIN: NULL;	BLOOD COAGULATION FACTOR BLOOD COAGULATION, GLYCOPROTEIN, CALCIUM, PLATELET, PLASMA, 2 ALTERNATIVE SPLICING, SIGNAL, DISEASE MUTATION, 3 POLYMORPHISM
1180	1fzc	B	148	416	1.7e-63			132.32	FIBRIN; CHAIN: A, B, C, D, E, F, G, H, I, J;	BLOOD COAGULATION BLOOD COAGULATION, PLASMA PROTEIN, CROSSLINKING
1180	1fze	C	151	422	3.4e-62			141.90	FIBRIN; CHAIN: A, B, C, D, E, F, G, H, I, J;	BLOOD COAGULATION BLOOD COAGULATION, PLASMA PROTEIN, CROSSLINKING
1180	1fzd	A	242	419	1.7e-57			154.36	FIBRINOGEN-420; CHAIN: A, B, C, D, E, F, G, H;	BLOOD COAGULATION BLOOD COAGULATION, FIBRINOGEN-420, ALPHAECDOMAIN, 2 FIBRINOGEN RELATED DOMAIN, GLYCOSYLATED PROTEIN
1180	1fzg	C	170	419	1.1e-39			141.24	FIBRINOGEN; CHAIN: A, B, C, D, E, F, S, T, M, N;	BLOOD COAGULATION BLOOD COAGULATION, PLASMA, PLATELET, FIBRINOGEN, FIBRIN
1180	1fzg	E	160	416	3.2e-39			130.27	FIBRINOGEN; CHAIN: A, B, C,	BLOOD COAGULATION BLOOD

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									D, E, F, S, T, M, N;	COAGULATION, PLASMA, PLATELET, FIBRINOGEN, FIBRIN
1181	1fim		2	104	1.6e-43			145.02	MACROPHAGE MIGRATION INHIBITORY FACTOR; CHAIN: NULL;	CYTOKINE MACROPHAGE, INFLAMMATORY RESPONSE, CYTOKINE
1181	1gif	A	1	115	1.6e-52			180.54	GLYCOSYLATION-INHIBITING FACTOR; CHAIN: A, B, C;	CYTOKINE MACROPHAGE, INFLAMMATORY RESPONSE, CYTOKINE
1181	1mfi	A	2	115	3.2e-52			170.94	MACROPHAGE MIGRATION INHIBITORY FACTOR; CHAIN: A, B, C;	CYTOKINE PHENYLPYRUVATE TAUTOMERASE; CYTOKINE, MACROPHAGE, INFLAMMATORY RESPONSE, TAUTOMERASE
1185	1d2n	A	195	450	1.2e-35			76.43	N-ETHYLMALEIMIDE-SENSITIVE FUSION PROTEIN; CHAIN: A;	HEXAMERIZATION DOMAIN, HEXAMERIZATION DOMAIN, ATPASE, TRANSPORT
1195	1a8y		382	723	4.8e-25			91.59	CALSEQUESTIN; CHAIN: NULL	CALCIUM-BINDING PROTEIN CALSEQUESTIN, CALCIUM-BINDING PROTEIN, SARCOPLASMIC 2 RETICULUM, RABBIT SKELETAL MUSCLE
1200	1ayz	A	31	190	3.2e-47			71.29	UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN CONJUGATION UBC2; UBIQUITIN CONJUGATION, UBIQUITIN-CONJUGATING ENZYME
1200	1c4z	D	47	191	9.6e-40			84.49	UBIQUITIN-PROTEIN LIGASE E3A; CHAIN: A, B, C; UBIQUITIN CONJUGATING ENZYME E2; CHAIN: D;	LIGASE E6AP; UBCH7; BILOBAL STRUCTURE, ELONGATED SHAPE, E3 UBIQUITIN LIGASE, E2 2 UBIQUITIN CONJUGATING ENZYME
1200	1qcq	A	44	193	3.2e-53			81.61	UBIQUITIN CONJUGATING ENZYME; CHAIN: A;	LIGASE UBIQUITIN, UBIQUITIN-CONJUGATING ENZYME, YEAST

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1200	1u9a	A	24	193	1.6e-43			74.19	UBC9; CHAIN: NULL;	UBIQUITIN-CONJUGATING ENZYME UBIQUITIN-CONJUGATING ENZYME; UBIQUITIN-CONJUGATING ENZYME, UBIQUITIN-DIRECTED 2 PROTEOLYSIS, CELL CYCLE CONTROL, LIGASE
1200	2aak		31	193	3.2e-47			71.32	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION UBC1; UBIQUITIN CONJUGATION, LIGASE
1200	2e2c		26	193	1.4e-41			67.54	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION, UBIQUITIN CARRIER PROTEIN, THIOESTER 2 BOND, LIGASE
1200	2ucz		33	193	3.2e-43			64.54	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION UBC7; UBIQUITIN CONJUGATION, LIGASE, YEAST
1204	1awj		241	317	3.2e-15	-0.35	0.06		ITK; CHAIN: NULL;	TRANSFERASE IL-2-INDUCIBLE T-CELL KINASE; TRANSFERASE, REGULATORY INTRAMOLECULAR COMPLEX, KINASE
1204	1aww		250	319	1.1e-13	0.55	0.58		BRUTON'S TYROSINE KINASE; CHAIN: NULL;	TRANSFERASE ATK, AMGXI, BPK; TYROSINE KINASE, X-LINKED AGAMMAGLOBULINEMIA, XLA, BTK, SH3 2 DOMAIN, TRANSFERASE
1204	1bul	A	258	318	4.8e-15	0.03	0.21		HEMOPOIETIC CELL KINASE; CHAIN: A, B, C, D, E, F;	TRANSFERASE TYROSINE-PROTEIN KINASE, TRANSFERASE, SIGNAL TRANSDUCTION, 2 SH3
1204	1efn	A	258	317	1.6e-17	0.12	0.82		FYN TYROSINE KINASE; CHAIN: A, C; HIV-1 NEF PROTEIN; CHAIN: B, D;	COMPLEX (SH3 DOMAIN/VIRAL ENHANCER) SRC-HOMOLOGY 3 DOMAIN; COMPLEX (SH3 DOMAIN/VIRAL ENHANCER), PROTO-ONCOGENE, 2 TRANSFERASE, TYROSINE-

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										PROTEIN KINASE, PHOSPHORYLATION, 3 AIDS, MYRISTYLATION, GTP-BINDING, ATP-BINDING, SH3 DOMAIN, 4 SH2 DOMAIN, PPII HELIX, PXXP MOTIF
1204	1fyn	A	255	318	6.4e-19	0.32	0.58		PHOSPHOTRANSFERASE FYN; CHAIN: A; 3BP-2; CHAIN: B;	TRANSFERASE PROTO-ONCOGENE TYROSINE KINASE; PROTO-ONCOGENE, TRANSFERASE, TYROSINE-PROTEIN KINASE, 2 PHOSPHORYLATION, ATP-BINDING, MYRISTYLATION, SH3 DOMAIN, 3 COMPLEX (PHOSPHOTRANSFERASE/PEPTIDE)
1204	1gbr	A	260	322	4.8e-12	0.25	0.63		SIGNAL TRANSDUCTION PROTEIN GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (GRB2, N-TERMINAL 1GBR 3 SH3 DOMAIN) COMPLEXED WITH SOS-A PEPTIDE 1GBR 4 (NMR, 29 STRUCTURES) 1GBR 5	
1204	1nlo	C	259	316	1.3e-16	0.42	0.69		C-SRC; CHAIN: C; NL1 (MN7-MN2-MN1-PLPPLP); CHAIN: N;	COMPLEX (TRANSFERASE/PEPTIDE) SRC, SH3 DOMAIN, LIGANDS, NON-PEPTIDE ELEMENTS, 2 COMPLEX (TRANSFERASE/PEPTIDE)
1204	1qly	A	257	318	4.8e-13	0.41	0.43		TYROSINE-PROTEIN KINASE BTK; CHAIN: A;	TYROSINE-PROTEIN KINASE BRUTONS TYROSINE KINASE, B CELL PROGENITOR KINASE, TRANSFERASE, TYROSINE-PROTEIN KINASE, PHOSPHORYLATION, 2 SH3 DOMAIN
1204	1shf	A	256	318	8e-19	0.39	0.31		PHOSPHOTRANSFERASE FYN	

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1204	2abl		251	423	9.6e-28	0.04	-0.15		PROTO-ONCOGENE TYROSINE KINASE (E.C.2.7.1.112) ISHF 3 (SH3 DOMAIN) ISHF 4	
1204	4hck		255	318	3.2e-15	0.04	0.55		ABL TYROSINE KINASE; CHAIN: NULL;	TRANSFERASE TRANSFERASE, TYROSINE KINASE, SH3, SH2, ONCOPROTEIN
1205	1coy	A	38	98	0.0096	0.69	0.19		HEMATOPOIETIC CELL KINASE; CHAIN: NULL;	TRANSFERASE HCK; SH3, PROTEIN TYROSINE KINASE, SIGNAL TRANSDUCTION, 2 TRANSFERASE
1208	1cho	I	554	592	5.1e-07	-0.30	0.58		CYTOCHROME B5; CHAIN: A;	ELECTRON TRANSPORT HELIX, BETA-STRAND, ELECTRON TRANSPORT
1208	1ldt	L	559	587	1.7e-07	-0.23	0.86		COMPLEX(SERINE PROTEINASE-INHIBITOR) ALPHA-CHYMOTRYPSIN (E.C.3.4.21.1) COMPLEX WITH TURKEY 1CHO 4 OVOMUCOID THIRD DOMAIN (/OMTKY3\$) 1CHO 5	
1215	1ak8		356	410	3.4e-05	-0.15	0.05		TRYPSIN; CHAIN: T; TRYPTASE INHIBITOR; CHAIN: L;	COMPLEX (HYDROLASE/INHIBITOR) LDTI; COMPLEX (HYDROLASE/INHIBITOR), HYDROLASE, INHIBITOR, 2 INFLAMMATION, TRYPTASE
1215	1c7w	A	349	410	6.8e-06	-0.50	0.23		CALMODULIN; CHAIN: NULL;	CALCIUM-BINDING PROTEIN CALMODULIN CERUM TRIC- DOMAIN, RESIDUES 1 - 75; CERIUM-LOADED, CALCIUM-BINDING PROTEIN
									CALCIUM VECTOR PROTEIN;	METAL BINDING PROTEIN CAVP;

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1215	1cdm	A	356	418	3.4e-05	-0.48	0.09		CHAIN: A; CALCIUM-BINDING PROTEIN CALMODULIN COMPLEXED WITH CALMODULIN-BINDING DOMAIN OF 1CDM 3 CALMODULIN-DEPENDENT PROTEIN KINASE II 1CDM 4	EF-HAND FAMILY, CALCIUM BINDING PROTEIN, NMR
1215	1cho	I	39	84	5.1e-10	0.04	0.65		COMPLEX(SERINE PROTEINASE-INHIBITOR) ALPHA-CHYMOTRYPSIN (E.C.3.4.21.1) COMPLEX WITH TURKEY ICHO 4 OVOMUCOID THIRD DOMAIN (/OMTKY3\$) ICHO 5	
1215	1dtl	A	349	410	1.7e-05	-0.26	0.21		CARDIAC TROPONIN C; CHAIN: A;	STRUCTURAL PROTEIN HELIX-TURN-HELIX
1215	1exr	A	348	414	1.4e-05	0.15	0.05		CALMODULIN; CHAIN: A;	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER
1215	1ezg	A	226	305	3.2e-06	0.21	0.13		THERMAL HYSTERESIS PROTEIN ISOFORM YL-1; CHAIN: A, B;	ANTIFREEZE PROTEIN INSECT ANTIFREEZE PROTEIN, THERMAL HYSTERESIS, TENEBRIO 2 MOLITOR, IODINATION, RIGHT-HANDED BETA-HELIX, TMAFP
1215	1f71	A	349	410	6.8e-05	0.10	0.69		CALMODULIN; CHAIN: A;	TRANSPORT PROTEIN CALCIUM BINDING; EF HAND, FOUR-HELIX BUNDLE
1215	1fak	L	236	302	4.8e-09	0.07	-0.19		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
1215	1nub	A	201	426	1.7e-28			73.86	BASEMENT MEMBRANE PROTEIN BM-40; CHAIN: A, B;	EXTRACELLULAR MODULE OSTEOONECTIN, SPARC, SECRETED PROTEIN ACIDIC AND EXTRACELLULAR MODULE, GLYCOPROTEIN, ANTI-ADHESIVE PROTEIN, 2 COLLAGEN BINDING, SITE-DIRECTED MUTAGENESIS, GLYCOSYLATED 3 PROTEIN MODRES
1215	1qjt	A	348	419	6.8e-07	-0.05	0.01		EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE CHAIN: A;	GROWTH FACTOR EHI; EH DOMAIN, EPS15, EF-HAND, SOLUTION STRUCTURE, S100 PROTEIN
1215	1rro		348	410	3.4e-05	-0.37	0.19		CALCIUM-BINDING PROTEIN RAT ONCOMODULIN 1RRO 3	
1215	1sgp	I	43	84	1.7e-08	0.67	0.55		STREPTOMYCES GRISEUS PROTEINASE B; 1SGP 6 CHAIN: E; 1SGP 7 TURKEY OVOMUCOID INHIBITOR; 1SGP 11 CHAIN: I; 1SGP 12	COMPLEX (SERINE PROTEASE/INHIBITOR) SGPB; 1SGP 8 ALA18-OMTKY3; 1SGP 14 SERINE PROTEINASE, PROTEIN INHIBITOR 1SGP 25
1215	1sra		279	423	1.5e-38	0.43	0.72		SPARC; 1SRA 4 CHAIN: NULL; 1SRA 5	CALCIUM-BINDING PROTEIN BM-40, OSTEOONECTIN; 1SRA 7 EXTRACELLULAR MATRIX PROTEIN 1SRA 20
1215	1sra		279	426	1.5e-38			58.51	SPARC; 1SRA 4 CHAIN: NULL; 1SRA 5	CALCIUM-BINDING PROTEIN BM-40, OSTEOONECTIN; 1SRA 7 EXTRACELLULAR MATRIX PROTEIN 1SRA 20
1215	1xka	L	240	313	4.8e-09	0.09	-0.19		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1215	3ovo		40	84	1.7e-09	0.76	0.21		PROTEINASE INHIBITOR (KAZAL) OVOMUCOID THIRD DOMAIN CLEAVED RDI 3OVO 3	GROWTH FACTOR LIKE DOMAIN
1215	5pal		348	410	3.4e-05	-0.11	0.13		CALCIUM-BINDING PROTEIN PARVALBUMIN (ALPHA LINEAGE) 5PAL 3	
1215	9wga	A	112	286	3.2e-15	0.08	-0.19		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
1216	1a8a		1	217	3.2e-51	0.58	1.00		ANNEXIN V; CHAIN: NULL;	PHOSPHOLIPID ANALOG PLACENTAL ANTICOAGULANT PROTEIN; PHOSPHOLIPID ANALOG, CALCIUM BINDING PROTEIN, MEMBRANE 2 BINDING PROTEIN
1216	1a8a		1	217	3.2e-51			75.48	ANNEXIN V; CHAIN: NULL;	PHOSPHOLIPID ANALOG PLACENTAL ANTICOAGULANT PROTEIN; PHOSPHOLIPID ANALOG, CALCIUM BINDING PROTEIN, MEMBRANE 2 BINDING PROTEIN
1216	1ain		61	222	1e-68	0.23	1.00		CALCIUM/PHOSPHOLIPID BINDING ANNEXIN I 1AIN 3	
1216	1ain		61	223	1e-68			170.55	CALCIUM/PHOSPHOLIPID BINDING ANNEXIN I 1AIN 3	
1216	1ain		62	222	4.8e-67	-0.02	1.00		CALCIUM/PHOSPHOLIPID BINDING ANNEXIN I 1AIN 3	
1216	1ala		1	214	3.2e-53	0.42	1.00		CALCIUM/PHOSPHOLIPID-BINDING PROTEIN ANNEXIN V 1ALA 3	
1216	1ala		1	214	3.2e-53			75.25	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN ANNEXIN V 1ALA 3	

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1216	1ann		11	215	9.6e-51	0.42	1.00		ANNEXIN IV; 1ANN 5 CHAIN: NULL; 1ANN 6	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN 32.5 KD CALECTRIN, ENDONEXIN I; 1ANN 7 32.5KD CALECTRIN, ENDONEXIN I, LIPOCORTIN IV, 1ANN 12 2 CHROMOBINDIN IV, PROTEIN II 1ANN 13
1216	1ann		1	216	3.2e-67			68.51	ANNEXIN IV; 1ANN 5 CHAIN: NULL; 1ANN 6	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN 32.5 KD CALECTRIN, ENDONEXIN I; 1ANN 7 32.5KD CALECTRIN, ENDONEXIN I, LIPOCORTIN IV, 1ANN 12 2 CHROMOBINDIN IV, PROTEIN II 1ANN 13
1216	1ann		62	219	3.2e-67	0.46	1.00		ANNEXIN IV; 1ANN 5 CHAIN: NULL; 1ANN 6	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN 32.5 KD CALECTRIN, ENDONEXIN I; 1ANN 7 32.5KD CALECTRIN, ENDONEXIN I, LIPOCORTIN IV, 1ANN 12 2 CHROMOBINDIN IV, PROTEIN II 1ANN 13
1216	1avc		10	216	1.6e-50	0.24	1.00		ANNEXIN VI; CHAIN: NULL;	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN P68, PROTEIN III, 67-KDA-CALCIMEDIN, LIPOCORTIN ANNEXIN, CALCIUM-BINDING, MEMBRANE-BINDING, 2
1216	1avc		5	221	9.6e-78	0.48	1.00		ANNEXIN VI; CHAIN: NULL;	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN P68, PROTEIN III, 67-KDA-CALCIMEDIN, LIPOCORTIN ANNEXIN, CALCIUM-BINDING, MEMBRANE-BINDING, 2

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1216	1axn		4	216	9.6e-53	0.76	1.00		ANNEXIN III; 1AXN 4 CHAIN: NULL; 1AXN 5	PROTEIN CALCIUM/PHOSPHOLIPID-BINDING PROTEIN ANNEXIN FAMILY 1AXN 14
1216	1axn		53	223	3.2e-67			84.90	ANNEXIN III; 1AXN 4 CHAIN: NULL; 1AXN 5	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN ANNEXIN FAMILY 1AXN 14
1216	1axn		59	222	3.2e-67	0.70	1.00		ANNEXIN III; 1AXN 4 CHAIN: NULL; 1AXN 5	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN ANNEXIN FAMILY 1AXN 14
1216	lhvd		1	212	1.1e-49			69.28	CALCIUM/PHOSPHOLIPID BINDING ANNEXIN V (LIPOCORTIN V, ENDONEXIN II, PLACENTAL 1HVD 3 ANTICOAGULANT PROTEIN) (CALCIUM IONS ARE VISIBLE) (MUTATION 1HVD 4 WITH GLU 17 REPLACED BY GLY (E17G) 1HVD 5	
1217	1a8a		8	189	8e-39	0.64	1.00		ANNEXIN V; CHAIN: NULL;	PHOSPHOLIPID ANALOG PLACENTAL ANTICOAGULANT PROTEIN; PHOSPHOLIPID ANALOG, CALCIUM BINDING PROTEIN, MEMBRANE 2 BINDING PROTEIN
1217	1ain		13	187	8e-32	0.22	1.00		CALCIUM/PHOSPHOLIPID BINDING ANNEXIN I 1AIN 3	
1217	1ain		33	304	0			403.43	CALCIUM/PHOSPHOLIPID BINDING ANNEXIN I 1AIN 3	
1217	1ain		35	300	0	0.17	1.00		CALCIUM/PHOSPHOLIPID BINDING ANNEXIN I 1AIN 3	
1217	1ala		8	186	3.2e-38	0.31	1.00		CALCIUM/PHOSPHOLIPID-BINDING PROTEIN ANNEXIN V 1ALA 3	

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1217	1ann		8	187	3.2e-38	0.55	1.00		ANNEXIN IV; 1ANN 5 CHAIN: NULL; 1ANN 6	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN 32.5 KD CALECTRIN, ENDONEXIN I; 1ANN 7 32.5KD CALECTRIN, ENDONEXIN I, LIPOCORTIN IV, 1ANN 12 2 CHROMOBINDIN IV, PROTEIN II 1ANN 13
1217	1avc		8	186	4.8e-26	0.28	1.00		ANNEXIN VI; CHAIN: NULL;	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN P68, PROTEIN III, 67-KDA-CALCIMEDIN, LIPOCORTIN ANNEXIN, CALCIUM-BINDING, MEMBRANE-BINDING, 2 CALCIUM/PHOSPHOLIPID-BINDING PROTEIN
1217	1axn		8	187	1.6e-37	0.54	1.00		ANNEXIN III; 1AXN 4 CHAIN: NULL; 1AXN 5	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN ANNEXIN FAMILY 1AXN 14
1217	1hvd		8	184	6.4e-38	0.31	1.00		CALCIUM/PHOSPHOLIPID BINDING ANNEXIN V (LIPOCORTIN V, ENDONEXIN II, PLACENTAL IHVD 3 ANTICOAGULANT PROTEIN) (CALCIUM IONS ARE VISIBLE) MUTATION IHVD 4 WITH GLU 17 REPLACED BY GLY (E17G) IHVD 5	
1218	1a8a		31	195	3.2e-66			58.84	ANNEXIN V; CHAIN: NULL;	PHOSPHOLIPID ANALOG PLACENTAL ANTICOAGULANT PROTEIN; PHOSPHOLIPID ANALOG, CALCIUM BINDING PROTEIN, MEMBRANE 2 BINDING PROTEIN
1218	1a8a		33	194	3.2e-66	0.68	1.00		ANNEXIN V; CHAIN: NULL;	PHOSPHOLIPID ANALOG PLACENTAL ANTICOAGULANT

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										PROTEIN; PHOSPHOLIPID ANALOG, CALCIUM BINDING PROTEIN, MEMBRANE 2 BINDING PROTEIN
1218	1ain		33	194	1e-68	0.23	1.00		CALCIUM/PHOSPHOLIPID BINDING ANNEXIN I IAIN 3	
1218	1ain		33	195	1e-68			170.39	CALCIUM/PHOSPHOLIPID BINDING ANNEXIN I IAIN 3	
1218	1ain		35	194	1.6e-65	0.15	1.00		CALCIUM/PHOSPHOLIPID BINDING ANNEXIN I IAIN 3	
1218	1ann		33	195	3.2e-68			65.05	ANNEXIN IV; IANN 5 CHAIN; NULL; IANN 6	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN 32.5 KD CALECTRIN, ENDONEXIN I; IANN 7 32.5KD CALECTRIN, ENDONEXIN I, LIPOCORTIN IV, IANN 12 2 CHROMOBINDIN IV, PROTEIN II IANN 13
1218	1ann		34	190	3.2e-68	0.54	1.00		ANNEXIN IV; IANN 5 CHAIN; NULL; IANN 6	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN 32.5 KD CALECTRIN, ENDONEXIN I; IANN 7 32.5KD CALECTRIN, ENDONEXIN I, LIPOCORTIN IV, IANN 12 2 CHROMOBINDIN IV, PROTEIN II IANN 13
1218	1avc		2	186	1.6e-38	0.30	1.00		ANNEXIN VI; CHAIN: NULL;	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN P68, PROTEIN III, 67-KDA-CALCIMEDIN, LIPOCORTIN ANNEXIN, CALCIUM-BINDING, MEMBRANE-BINDING, 2 CALCIUM/PHOSPHOLIPID-BINDING PROTEIN
1218	1avc		34	193	1.6e-71	0.61	1.00		ANNEXIN VI; CHAIN: NULL;	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN P68, PROTEIN III, 67-KDA-CALCIMEDIN, LIPOCORTIN ANNEXIN, CALCIUM-BINDING,

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										MEMBRANE-BINDING, 2 CALCIUM/PHOSPHOLIPID-BINDING PROTEIN
1218	1axn		25	195	6.4e-67			85.90	ANNEXIN III; 1AXN 4 CHAIN: NULL; 1AXN 5	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN ANNEXIN FAMILY 1AXN 14
1218	1axn		31	194	6.4e-67	0.70	1.00		ANNEXIN III; 1AXN 4 CHAIN: NULL; 1AXN 5	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN ANNEXIN FAMILY 1AXN 14
1218	1dk5	A	2	169	3.2e-19	0.02	1.00		ANNEXIN 24(CA32); CHAIN: A, B;	METAL BINDING PROTEIN PLANT ANNEXIN, CAPSICUM ANNUUM, BELL PEPPER, CALCIUM 2 BINDING PROTEIN
1218	1hvd		32	195	9.6e-68			68.02	CALCIUM/PHOSPHOLIPID BINDING ANNEXIN V (LIPOCORTIN V, ENDONEXIN II, PLACENTAL IHVD 3 ANTICOAGULANT PROTEIN) (CALCIUM IONS ARE VISIBLE) MUTATION IHVD 4 WITH GLU 17 REPLACED BY GLY (E17G) IHVD 5	
1218	1hvd		33	194	9.6e-68	0.59	1.00		CALCIUM/PHOSPHOLIPID BINDING ANNEXIN V (LIPOCORTIN V, ENDONEXIN II, PLACENTAL IHVD 3 ANTICOAGULANT PROTEIN) (CALCIUM IONS ARE VISIBLE) MUTATION IHVD 4 WITH GLU 17 REPLACED BY GLY (E17G) IHVD 5	
1219	1b3u	A	23	627	1.6e-45			120.56	PROTEIN PHOSPHATASE PP2A; CHAIN: A, B;	SCAFFOLD PROTEIN SCAFFOLD PROTEIN, PP2A,

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1219	1b3u	A	320	643	1.6e-09	0.07	0.23		PROTEIN PHOSPHATASE PP2A; CHAIN: A, B;	PHOSPHORYLATION, HEAT REPEAT SCAFFOLD PROTEIN SCAFFOLD PROTEIN, PP2A, PHOSPHORYLATION, HEAT REPEAT SCAFFOLD PROTEIN SCAFFOLD PROTEIN, PP2A, PHOSPHORYLATION, HEAT REPEAT
1219	1b3u	A	71	625	1.6e-45	0.04	-0.07		PROTEIN PHOSPHATASE PP2A; CHAIN: A, B;	PHOSPHORYLATION, HEAT REPEAT SCAFFOLD PROTEIN SCAFFOLD PROTEIN, PP2A, PHOSPHORYLATION, HEAT REPEAT
1219	1ee4	A	211	473	1.7e-10	0.36	1.00		KARYOPHERIN ALPHA; CHAIN: A, B; MYC PROTO-ONCOGENE PROTEIN; CHAIN: C, D, E, F;	TRANSPORT PROTEIN SERINE-RICH RNA POLYMERASE I SUPPRESSOR PROTEIN; ARM REPEAT
1219	1ee4	A	279	643	1.4e-44	0.57	0.86		KARYOPHERIN ALPHA; CHAIN: A, B; MYC PROTO-ONCOGENE PROTEIN; CHAIN: C, D, E, F;	TRANSPORT PROTEIN SERINE-RICH RNA POLYMERASE I SUPPRESSOR PROTEIN; ARM REPEAT
1219	1ial	A	179	628	1.3e-43			118.96	IMPORTIN ALPHA; CHAIN: A;	NUCLEAR IMPORT RECEPTOR KARYOPHERIN ALPHA; NUCLEAR IMPORT RECEPTOR, NUCLEAR LOCALIZATION SIGNAL, 2 ARMADILLO REPEATS, AUTOINHIBITION, INTRASTERIC REGULATION
1219	1ial	A	272	643	1.3e-43	0.50	0.53		IMPORTIN ALPHA; CHAIN: A;	NUCLEAR IMPORT RECEPTOR KARYOPHERIN ALPHA; NUCLEAR IMPORT RECEPTOR, NUCLEAR LOCALIZATION SIGNAL, 2 ARMADILLO REPEATS, AUTOINHIBITION, INTRASTERIC REGULATION
1219	1ibr	B	318	633	4.8e-15	0.01	-0.15		RAN; CHAIN: A, C; IMPORTIN BETA SUBUNIT; CHAIN: B, D;	SMALL GTPASE KARYOPHERIN BETA, P95 SMALL GTPASE, NUCLEAR TRANSPORT RECEPTOR
1219	2bct		239	643	1.1e-39	0.51	0.06		BETA-CATENIN; CHAIN: NULL;	STRUCTURAL PROTEIN ARMADILLO REPEAT, BETA-

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1219	3bct		277	643	3.2e-35	0.46	0.24		BETA-CATENIN; CHAIN: NULL;	CATENIN, STRUCTURAL PROTEIN ARMADILLO REPEAT ARMADILLO REPEAT, BETA-CATENIN, CYTOSKELETON
1221	1bu7	A	19	486	9.6e-53			174.17	CYTOCHROME P450; CHAIN: A, B;	OXIDOREDUCTASE FATTY ACID HYDROXYLASE; FATTY ACID MONOOXYGENASE, HEMOPROTEIN, P450 REMARK
1221	1oxa		27	486	3.2e-24			94.76	CYTOCHROME P450 ERYF; 10XA 5 CHAIN: NULL 10XA 6	OXIDOREDUCTASE (OXYGENASE)
1222	1bu7	A	35	324	1.3e-18	-0.20	0.04		CYTOCHROME P450; CHAIN: A, B;	OXIDOREDUCTASE FATTY ACID HYDROXYLASE; FATTY ACID MONOOXYGENASE, HEMOPROTEIN, P450 REMARK
1222	1bu7	A	61	318	3.4e-36	-0.23	0.29		CYTOCHROME P450; CHAIN: A, B;	OXIDOREDUCTASE FATTY ACID HYDROXYLASE; FATTY ACID MONOOXYGENASE, HEMOPROTEIN, P450 REMARK
1222	1dt6	A	31	325	3.2e-92	-0.02	0.99		CYTOCHROME P450 2C5; CHAIN: A;	OXIDOREDUCTASE PROGESTERONE 21-HYDROXYLASE, CYPIC5 P450 1, MEMBRANE PROTEIN, PROGESTERONE 21-HYDROXYLASE, BENZO(A) 2 PYRENE HYDROXYLASE, ESTRADIOL 2-HYDROXYLASE, P450, CYP2C5
1222	1f26	A	48	318	1.7e-21	-0.08	0.05		NITRIC OXIDE REDUCTASE; CHAIN: A;	OXIDOREDUCTASE NITRIC OXIDE REDUCTASE, CYTOCHROME P450NOR
1222	1oxa		61	318	6.8e-33	-0.40	0.28		CYTOCHROME P450 ERYF; 10XA 5 CHAIN: NULL 10XA 6	OXIDOREDUCTASE (OXYGENASE)

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1227	1ctz	A	130	352	0.00032	-0.06	0.04		TOLB PROTEIN; CHAIN: A;	TOXIN BINDING PROTEIN TWO DOMAINS: BETA PROPELLER AND ALPHA/BETA FOLD
1227	1erj	A	116	431	4.8e-73	0.57	1.00		TRANSCRIPTIONAL REPRESSOR TUPI; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
1227	1erj	A	4	285	1.3e-58	0.40	0.29		TRANSCRIPTIONAL REPRESSOR TUPI; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
1227	1erj	A	65	373	1.6e-66	0.38	1.00		TRANSCRIPTIONAL REPRESSOR TUPI; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
1227	1got	B	12	370	1.3e-77			119.11	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
1227	1got	B	14	328	1.3e-77	0.14	0.53		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
1227	1got	B	166	431	4.8e-54	0.64	1.00		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										BINDING/TRANSDUCER, G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
1235	1aif	H	413	518	0.0068	-0.14	0.35		ANTI-IDIOTYPIC FAB 409.5.3 (IGG2A) FAB; CHAIN: A, B, L, H	IMMUNOGLOBULIN IMMUNOGLOBULIN, C REGION, V REGION
1235	1qun	B	321	580	1.2e-15	-0.00	-0.18		PAPD-LIKE CHAPERONE FIMC; CHAIN: A, C, E, G, I, K, M, O; MANNOSE-SPECIFIC ADHESIN FIMH; CHAIN: B, D, F, H, J, L, N, P;	CHAPERONE/STRUCTURAL PROTEIN CHAPERONE ADHESIN DONOR STRAND COMPLEMENTATION, 2 CHAPERONE/STRUCTURAL PROTEIN
1235	1qun	B	408	701	6.8e-16	0.11	-0.19		PAPD-LIKE CHAPERONE FIMC; CHAIN: A, C, E, G, I, K, M, O; MANNOSE-SPECIFIC ADHESIN FIMH; CHAIN: B, D, F, H, J, L, N, P;	CHAPERONE/STRUCTURAL PROTEIN CHAPERONE ADHESIN DONOR STRAND COMPLEMENTATION, 2 CHAPERONE/STRUCTURAL PROTEIN
1236	1fs2	A	214	293	0.00034	-0.25	0.13		SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	LIGASE CYCLIN A/CDK2-ASSOCIATED P45; CYCLIN A/CDK2-ASSOCIATED P19; SKP1, SKP2, I-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
1236	1pjr		430	960	3.2e-68	-0.22	0.58		PCRA; CHAIN: NULL;	HELICASE DNA REPAIR, DNA REPLICATION, SOS RESPONSE, HELICASE, 2 ATP-BINDING, DNA-BINDING
1236	1uaa	A	441	872	1.6e-47	-0.55	0.00		ATP-DEPENDENT DNA HELICASE REP; CHAIN: A, B; DNA CHAIN: C;	COMPLEX (HELICASE/DNA) COMPLEX (HELICASE/DNA), HELICASE, DNA UNWINDING
1236	2pjr	A	436	991	1.3e-62			90.62	HELICASE PCRA; CHAIN: A, F;	HYDROLASE/DNA ATP-DEPENDENT

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									HELICASE PCRA; CHAIN: B, G; DNA (5'-D(*Tp*Tp*Tp*Tp*3'); CHAIN: C, D; DNA (5'-D(*Gp*C)-3'); CHAIN: H; DNA (5'-D(*Ap* Cp*Tp*Gp*C)-3'); CHAIN: I;	HELICASE PCRA; ATP-DEPENDENT HELICASE PCRA; HELICASE PCRA, HYDROLASE, DNA, PRODUCT COMPLEX
1237	1a4y	A	10	213	3.4e-22	-0.01	0.89		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS
1237	1a4y	A	126	299	6.4e-07	0.04	0.09		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS
1237	1a9n	A	12	151	3.4e-13	0.04	0.35		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1237	1a9n	A	20	101	3.2e-07	0.28	0.51		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1237	1a9n	A	51	187	8.5e-24	0.36	0.71		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1237	1a9n	A	72	196	3.4e-20	0.04	0.04		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1237	1a9n	C	20	101	3.2e-07	0.49	0.35		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	SNRNP-RIBONUCLEOPROTEIN COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP-RIBONUCLEOPROTEIN
1237	1a9n	C	51	192	5.1e-24	0.05	0.66		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP-RIBONUCLEOPROTEIN
1237	1d0b	A	3	187	3.2e-25	-0.14	0.71		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1237	1d0b	A	44	221	6.8e-29	-0.20	0.07		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1237	1d0b	A	75	268	6.4e-21	0.15	-0.02		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1237	1dce	A	11	100	1.6e-11	0.35	0.96		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1237	1dce	A	130	233	3.2e-13	0.47	0.94		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1237	1dce	A	160	278	4.8e-10	0.20	-0.03		RAB GERANYLGERANYLTRANSFERASE	TRANSFERASE CRYSTAL STRUCTURE, RAB

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									RASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFE RASE BETA SUBUNIT; CHAIN: B, D;	GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N- FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1237	1dce	A	44	169	3.2e-11	0.21	0.33		RAB GERANYLGERANYLTRANSFE RASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFE RASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N- FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1237	1ds9	A	11	146	4.8e-12	-0.31	0.09		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE- RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1237	1ds9	A	130	252	3.2e-14	-0.20	0.22		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE- RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1237	1ds9	A	37	169	1.6e-11	-0.54	0.45		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE- RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1237	1fo1	A	132	192	1.1e-06	-0.03	0.65		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH- REPEAT 2 (LRR)
1237	1fo1	B	132	192	1.1e-06	0.25	0.60		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH- REPEAT 2 (LRR)
1237	1fs2	A	10	206	1.2e-25	0.15	0.46		SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	LIGASE CYCLIN A/CDK2- ASSOCIATED P45; CYCLIN A/CDK2-

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
1237	1fs2	A	130	294	1.1e-06	0.34	0.22		SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	LIGASE CYCLIN A/CDK2-ASSOCIATED P45; CYCLIN A/CDK2-ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
1237	2bnh		19	223	1.5e-28	-0.03	0.82		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1238	1a17		119	279	1e-18	0.10	0.80		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
1238	1a17		133	250	6.4e-14	0.27	0.51		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
1238	1a17		153	296	4.8e-13	0.30	0.76		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
1238	1a17		20	153	8e-13	0.01	0.23		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1238	1a17		221	368	5.1e-19	0.31	0.99		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	STRUCTURE HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY
1238	1a17		232	348	9.6e-13	0.56	0.94		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	STRUCTURE HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY
1238	1a17		263	392	9.6e-13	0.22	0.80		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	STRUCTURE HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY
1238	1a17		290	416	3.2e-14	0.22	0.52		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	STRUCTURE HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY
1238	1a17		29	142	1.7e-15	0.18	0.11		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	STRUCTURE HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY
1238	1a17		300	414	1.7e-18	-0.14	0.74		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	STRUCTURE HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY
1238	1a17		338	421	4.8e-13	0.41	0.37		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	STRUCTURE HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1238	1a17		56	184	1.7e-15	0.18	0.70		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
1238	1a17		63	175	8e-10	0.34	0.41		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
1238	1a17		85	209	4.8e-11	0.12	0.58		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
1238	1a17		89	212	3.4e-17	0.12	0.65		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
1238	1d8d	A	217	410	4.8e-07	-0.23	0.60		FARNESYLTRANSFERASE (ALPHA SUBUNIT); CHAIN: A; FARNESYLTRANSFERASE (BETA SUBUNIT); CHAIN: B; K-RAS4B PEPTIDE SUBSTRATE; CHAIN: P;	TRANSFERASE FTASE; FTASE; FTASE, PFT, PFTASE, FARNESYLTRANSFERASE, FARNESYL 2 TRANSFERASE, CAAX, RAS, CANCER
1238	1d8d	A	28	266	3.4e-15	-0.04	0.18		FARNESYLTRANSFERASE (ALPHA SUBUNIT); CHAIN: A; FARNESYLTRANSFERASE (BETA SUBUNIT); CHAIN: B; K-RAS4B PEPTIDE SUBSTRATE; CHAIN: P;	TRANSFERASE FTASE; FTASE; FTASE, PFT, PFTASE, FARNESYLTRANSFERASE, FARNESYL 2 TRANSFERASE, CAAX, RAS, CANCER

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1238	1e96	B	135	278	1.4e-09	0.15	0.48		RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	SIGNALLING COMPLEX RAC1; P67PHOX; SIGNALLING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF
1238	1e96	B	189	322	8e-10	0.40	0.76		RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	SIGNALLING COMPLEX RAC1; P67PHOX; SIGNALLING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF
1238	1e96	B	229	379	4.8e-09	0.14	0.98		RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	SIGNALLING COMPLEX RAC1; P67PHOX; SIGNALLING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF
1238	1e96	B	290	417	4.8e-09	0.05	0.86		RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	SIGNALLING COMPLEX RAC1; P67PHOX; SIGNALLING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF
1238	1e96	B	62	244	0.00016	0.12	0.21		RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	SIGNALLING COMPLEX RAC1; P67PHOX; SIGNALLING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF
1238	1elr	A	133	247	6.4e-15	0.38	0.47		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1238	1elr	A	161	252	6.4e-15	0.24	1.00		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1238	1elr	A	195	283	1.6e-10	0.02	0.96		TPR2A-DOMAIN OF HOP;	CHAPERONE HOP, TPR-DOMAIN,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1238	1elr	A	228	326	4.8e-12	0.47	0.99		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1238	1elr	A	262	355	3.2e-13	0.27	0.74		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1238	1elr	A	28	117	4.8e-11	0.13	0.29		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1238	1elr	A	334	419	4.8e-12	0.54	0.55		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1238	1elr	A	93	185	1.1e-11	0.31	0.33		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1238	1elw	A	135	221	1.1e-13	0.46	0.99		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1238	1elw	A	153	262	1.3e-12	0.47	0.96		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1238	1elw	A	196	296	3.2e-10	0.63	1.00		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1238	1elw	A	236	332	4.8e-13	0.76	1.00		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	BINDING CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1238	1elw	A	25	122	4.8e-10	0.32	0.57		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1238	1elw	A	2	99	6.4e-14	0.25	0.03		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1238	1elw	A	304	408	3.2e-15	0.23	0.98		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1238	1elw	A	342	419	1.1e-11	0.29	0.21		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1238	1elw	A	61	155	6.4e-10	0.32	0.82		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1238	1fch	A	166	413	9.6e-38	0.32	1.00		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOMAL RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
1238	1fch	A	313	420	3.2e-09	0.07	0.96		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING	SIGNALING PROTEIN PEROXISOMAL RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									PEPTIDE; CHAIN: C, D;	PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
1238	1fch	A	34	273	6.4e-31	0.48	1.00		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOMORE RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
1238	1fch	A	7	220	1.3e-29	0.38	1.00		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOMORE RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
1238	1fch	A	98	345	4.8e-29	0.46	1.00		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOMORE RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
1241	1edh	A	34	152	3.2e-20	0.10	0.55		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
1241	1edh	A	52	253	6.8e-27	-0.19	0.76		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
1241	1edh	A	83	255	4.8e-17	0.21	0.64		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
1241	Inci	B	206	253	5.1e-06	-0.07	0.04		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
1241	Inci	B	56	152	1.7e-05	0.15	0.31		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
1241	Incj	A	34	152	1.4e-21	-0.20	0.28		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
1241	Incj	A	43	253	1.7e-21	-0.03	0.65		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
1241	Incj	A	90	255	6.4e-17	-0.20	0.35		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
1241	Iqu0	A	358	549	3.4e-20	-0.08	0.40		LAMININ ALPHA2 CHAIN; CHAIN: A, B, C, D;	METAL BINDING PROTEIN BETA SANDWICH, CALCIUM-BINDING PROTEIN, METAL BINDING 2 PROTEIN
1241	Isuh		43	154	1.7e-07	-0.22	0.04		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
1246	1a5e		132	262	3.4e-30	0.56	1.00		TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
1246	1a5e		166	330	3.4e-30	0.40	1.00		TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
1246	1a5e		202	359	5.1e-29	0.84	1.00		TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
1246	1a5e		233	385	1.5e-29	0.39	0.93		TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
1246	1a5e		233	393	3.4e-30			66.97	TUMOR SUPPRESSOR	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE, REPEAT, ANK REPEAT
1246	lawc	B	145	298	1e-43	1.05	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA I; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1246	lawc	B	14	165	1e-39	0.93	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA I; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1246	lawc	B	150	298	9.6e-41	0.97	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA I; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1246	lawc	B	17	165	1.6e-38	0.93	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA I; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1246	1awc	B	183	332	3.4e-39	0.84	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1246	1awc	B	184	332	9.6e-35	0.55	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1246	1awc	B	212	362	1e-40	0.77	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1246	1awc	B	212	363	1e-43			90.97	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1246	1awc	B	217	395	3.2e-32	0.21	0.23		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA;

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1246	1awc	B	3	132	1.6e-33	0.88	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1246	1awc	B	45	199	8.5e-39	0.55	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1246	1awc	B	50	199	9.6e-37	0.68	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1246	1bd8		145	301	8e-30			87.65	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1246	1bd8		153	301	8e-30	0.38	1.00		P19INK4D CDK4/6 INHIBITOR;	TUMOR SUPPRESSOR TUMOR

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									CHAIN: NULL;	SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1246	1bi7	B	244	365	1.7e-28	0.57	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR; CHAIN: B;	COMPLEX (KINASE/ANTI-ONCOGENE) CDK6; P16INK4A, MTS1; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, MULTIPLE TUMOR SUPPRESSOR, 3 MTS1, COMPLEX (KINASE/ANTI-ONCOGENE) HEADER
1246	1blx	B	114	304	3.4e-38	0.10	0.10		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1246	1blx	B	13	170	1.7e-39	0.93	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1246	1blx	B	147	303	6.8e-40			78.94	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1246	1blx	B	183	338	3.4e-38	0.73	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1246	1blx	B	215	368	1.7e-38	0.89	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	(INHIBITOR PROTEIN/KINASE) COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1246	1blx	B	50	205	1.5e-38	0.70	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1246	1blx	B	82	237	6.8e-40	1.03	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1246	1bu9	A	144	310	6.8e-37	0.78	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1246	1bu9	A	150	303	1.6e-36	0.97	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1246	1bu9	A	17	170	9.6e-37	0.87	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Coumpound	PDB annotation
1246	1bu9	A	181	338	1e-35	0.61	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1246	1bu9	A	184	367	8e-33	0.25	0.99		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1246	1bu9	A	215	373	3.4e-35	0.63	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1246	1bu9	A	243	394	6.8e-33	0.79	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1246	1bu9	A	3	174	3.4e-37	0.47	0.51		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1246	1bu9	A	44	205	1.7e-39	0.94	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1246	1bu9	A	9	177	1.7e-39			89.81	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1246	lihb	A	150	302	6.4e-36	0.88	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	HORMONE/GROWTH FACTOR CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1246	lihb	A	17	169	3.2e-36	0.78	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1246	lihb	A	184	366	3.2e-32	0.28	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1246	lihb	A	81	236	3.2e-36			83.68	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1246	likn	D	12	186	4.8e-35	0.47	1.00		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1246	likn	D	179	346	1.6e-30	0.20	0.92		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1246	likn	D	212	404	1.6e-34	0.22	0.35		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1246	likn	D	45	232	8e-43	0.18	1.00		NF-KAPPA-B P65 SUBUNIT;	TRANSCRIPTION FACTOR P65;

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1246	likn	D	45	253	8e-43			80.97	NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1246	lmyo		12	130	9.6e-25			68.11	MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLTATION, NMR, ANK-REPEAT
1246	lnfi	E	113	311	1.7e-48	0.69	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1246	lnfi	E	11	186	1.4e-35	0.81	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1246	lnfi	E	143	338	5.1e-47	0.55	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1246	lnfi	E	177	367	1.7e-48	0.62	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1246	lnfi	E	178	346	4.8e-30	0.65	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1246	Infi	E	17	170	3.4e-38	0.85	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1246	Infi	E	210	404	9.6e-35	0.26	0.21		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1246	Infi	E	215	394	1.5e-44	0.53	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1246	Infi	E	43	238	1.7e-51	0.53	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1246	Infi	E	43	242	1.7e-51			89.07	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1246	Infi	E	44	232	1.6e-42	0.74	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1246	Infi	E	82	278	5.1e-50	0.66	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1246	1sw6	A	76	320	1.3e-21			60.99	REGULATORY PROTEIN SW16; CHAIN: A, B;	ANKYRIN 2 REPEAT HELIX
1246	1ycs	B	214	398	3.2e-18			69.71	P53; CHAIN: A; 53BP2; CHAIN: B;	TRANSCRIPTION REGULATION, ANKYRIN REPEATS, CELL-CYCLE COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS)
1250	1cun	A	375	591	5.1e-12	-0.03	0.29		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1250	1cun	A	436	651	5.1e-07	0.02	0.03		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1250	1hae		120	150	0.0051	0.07	0.11		HEREGULIN-ALPHA; CHAIN: NULL;	GROWTH FACTOR NEU DIFFERENTIATION FACTOR (RAT), ACETYLCHOLINE GROWTH FACTOR
1250	1hre		120	150	0.0051	0.13	0.25		GROWTH FACTOR HEREGULIN-ALPHA (EPIDERMAL GROWTH FACTOR-LIKE DOMAIN) 1HRE 3 (NMR, MINIMIZED AVERAGE STRUCTURE) 1HRE 4	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1252	1d4v	A	326	426	5.1e-10	0.10	-0.14		TNF-RELATED APOPTOSIS INDUCING LIGAND; CHAIN: B; DEATH RECEPTOR 5; CHAIN: A;	APOPTOSIS TRAIL; DR5; LIGAND-RECEPTOR COMPLEX, TRIMERIC JELLY-ROLL, TNF-R 2 SUPERFAMILY, APOPTOSIS
1252	1dan	L	351	449	8e-09	0.06	-0.13		BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DFFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
1252	1dx5	I	233	346	3.2e-12	0.02	-0.20		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
1252	1dx5	I	268	394	6.4e-15	0.03	-0.20		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
1252	1dx5	I	308	436	1.1e-12	0.10	-0.19		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1252	1emn		307	395	1.6e-13	0.24	0.04		FIBRILLIN; CHAIN: NULL;	ANTIFIBRINOLYTIC COMPLEX MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
1252	1emn		351	431	3.2e-10	0.08	-0.19		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
1252	1klo		225	419	8.5e-39	0.17	0.93		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1252	1klo		234	411	8.5e-39			132.10	LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1252	1klo		293	452	1.6e-20	0.40	0.51		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1252	1klo		358	496	3.2e-18	-0.00	-0.03		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1252	1pfx	L	351	441	3.2e-09	0.10	-0.17		FACTOR IXA; CHAIN: C, L,; D- PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3 GLYCOPROTEIN
1252	1skz		319	414	3.4e-17	0.34	-0.14		ANTISTASIN; CHAIN: NULL;	SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1252	1skz		355	425	5.1e-10	0.16	0.19		ANTISTASIN; CHAIN: NULL;	INHIBITOR, THROMBOSIS
1252	1xka	L	355	448	3.2e-09	0.14	-0.18		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	SERINE PROTEASE INHIBITOR; FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS
1252	4mt2		368	428	1.3e-09	-0.05	0.00		METALLOTHIONEIN METALLOTHIONEIN ISOFORM II 4MT2.3	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
1252	9wga	A	298	492	4.8e-15	0.04	-0.19		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA.3	
1253	1one	A	11	134	9.6e-61	0.25	1.00		ENOLASE; CHAIN: A, B;	LYASE 2-PHOSPHO-D-GLYCERATE HYDROLASE; LYASE, GLYCOLYSIS
1253	1pdz		11	137	8e-63	0.15	1.00		ENOLASE; IPDZ 4 CHAIN: NULL; IPDZ 5	LYASE (CARBON-OXYGEN) 2-PHOSPHO-D-GLYCERATE DEHYDRATASE; IPDZ 6
1256	1kpf		53	163	9.6e-41	0.96	1.00		PROTEIN KINASE C INTERACTING PROTEIN; CHAIN: NULL;	PROTEIN KINASE INHIBITOR PKCI-1, PROTEIN KINASE C INHIBITOR 1, HINT PROTEIN KINASE INHIBITOR, PKCI-1, HIT PROTEIN FAMILY, 2 HISTIDINE TRIAD PROTEIN FAMILY, NUCLEOTIDYL HYDROLASE, 3 NUCLEOTIDYL TRANSFERASE
1256	1kpf		53	163	9.6e-41			144.01	PROTEIN KINASE C	PROTEIN KINASE INHIBITOR PKCI-

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									INTERACTING PROTEIN; CHAIN: NULL;	1, PROTEIN KINASE C INHIBITOR 1, HINT PROTEIN KINASE INHIBITOR, PKCI-1, HIT PROTEIN FAMILY, 2 HISTIDINE TRIAD PROTEIN FAMILY, NUCLEOTIDYL HYDROLASE, 3 NUCLEOTIDYL TRANSFERASE
1256	4rhv		47	163	6.4e-41			147.29	HISTIDINE TRIAD NUCLEOTIDE-BINDING PROTEIN; CHAIN: NULL;	NUCLEOTIDE-BINDING PROTEIN HINT; NUCLEOTIDE-BINDING PROTEIN
1256	4rhv		52	163	6.4e-41	0.86	1.00		HISTIDINE TRIAD NUCLEOTIDE-BINDING PROTEIN; CHAIN: NULL;	NUCLEOTIDE-BINDING PROTEIN HINT; NUCLEOTIDE-BINDING PROTEIN
1257	1a5e		39	151	1.4e-21	0.27	0.48		TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
1257	1a5e		39	154	8e-26	0.80	1.00		TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
1257	1a5e		61	162	3.4e-25	0.65	1.00		TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
1257	1a5e		6	121	4.8e-18	0.16	0.40		TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
1257	1awc	B	39	164	6.4e-37	0.61	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANK YRIN REPEATS, TRANSCRIPTION 3 FACTOR

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1257	1awc	B	4	154	9.6e-40	0.40	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA) DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1257	1bd8		7	157	1.3e-31	0.48	1.00		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1257	1bi7	B	39	154	3.2e-26	0.62	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR; CHAIN: B;	COMPLEX (KINASE/ANTI-ONCOGENE) CDK6; P16INK4A, MTS1; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, MULTIPLE TUMOR SUPPRESSOR, 3 MTS1, COMPLEX (KINASE/ANTI-ONCOGENE) HEADER
1257	1bi7	B	6	121	8e-19	0.22	0.35		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR; CHAIN: B;	COMPLEX (KINASE/ANTI-ONCOGENE) CDK6; P16INK4A, MTS1; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, MULTIPLE TUMOR SUPPRESSOR, 3 MTS1, COMPLEX (KINASE/ANTI-ONCOGENE) HEADER
1257	1biX	B	39	164	1.7e-32	0.82	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1257	1blx	B	7	157	1.6e-30	0.38	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	(INHIBITOR PROTEIN/KINASE) COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1257	1bu9	A	6	159	8e-37	0.34	0.88		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1257	1d9s	A	39	154	1.6e-26	0.70	1.00		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
1257	1d9s	A	6	127	3.2e-20	0.42	0.95		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
1257	1dcq	A	2	91	6.4e-15	0.41	0.80		PYK2-ASSOCIATED PROTEIN BETA; CHAIN: A;	METAL BINDING PROTEIN ZINC-BINDING MODULE, ANKYRIN REPEATS, METAL BINDING PROTEIN
1257	1dcq	A	71	157	1.1e-17	0.05	0.99		PYK2-ASSOCIATED PROTEIN BETA; CHAIN: A;	METAL BINDING PROTEIN ZINC-BINDING MODULE, ANKYRIN REPEATS, METAL BINDING PROTEIN
1257	lihb	A	6	158	4.8e-36	0.52	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1257	lihb	A	73	163	8e-18	0.47	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1257	1ikn	D	4	162	8e-38	0.08	0.84		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1257	1myo		35	152	3.2e-26			52.27	MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLTATION, NMR, ANK-REPEAT
1257	1myo		40	156	3.2e-26	0.32	0.98		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLTATION, NMR, ANK-REPEAT
1257	1myo		5	106	6.4e-24	0.22	0.98		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLTATION, NMR, ANK-REPEAT
1257	1myo		74	164	1.1e-23	0.04	1.00		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLTATION, NMR, ANK-REPEAT
1257	1nfi	E	4	162	1.6e-38	0.39	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1257	lycs	B	12	95	1.4e-19	0.04	0.86		P53; CHAIN: A; 53BP2; CHAIN: B;	COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3
1257	lycs	B	39	154	1.6e-25	0.24	1.00		P53; CHAIN: A; 53BP2; CHAIN: B;	ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1257	1yes	B	73	161	1.6e-22	0.44	1.00		P53; CHAIN: A; 53BP2; CHAIN: B;	ONCOGENE/ANKYRIN REPEATS) COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS)
1258	1afb	1	3	183	3.4e-20			52.08	MANNOSE-BINDING PROTEIN-A; 1AFB 4 CHAIN: 1, 2, 3; 1AFB 5	LECTIN CL-QPDWG; 1AFB 7 C-TYPE LECTIN, CALCIUM-BINDING PROTEIN 1AFB 22
1258	1bj3	A	31	180	8e-34	0.42	0.11		COAGULATION FACTOR IX-BINDING PROTEIN A; CHAIN: A; COAGULATION FACTOR IX-BINDING PROTEIN B; CHAIN: B;	COLLAGEN BINDING PROTEIN IX-BP; IX-BP; COAGULATION FACTOR IX-BINDING, HETERODIMER, VENOM, HABU 2 SNAKE, C-TYPE LECTIN SUPERFAMILY, COLLAGEN BINDING PROTEIN
1258	1bj3	A	34	181	8e-34			61.48	COAGULATION FACTOR IX-BINDING PROTEIN A; CHAIN: A; COAGULATION FACTOR IX-BINDING PROTEIN B; CHAIN: B;	COLLAGEN BINDING PROTEIN IX-BP; IX-BP; COAGULATION FACTOR IX-BINDING, HETERODIMER, VENOM, HABU 2 SNAKE, C-TYPE LECTIN SUPERFAMILY, COLLAGEN BINDING PROTEIN
1258	1c3a	A	31	185	6.4e-28	0.20	0.89		FLAVOCETIN-A: ALPHA SUBUNIT; CHAIN: A; FLAVOCETIN-A: BETA SUBUNIT; CHAIN: B	MEMBRANE PROTEIN C-TYPE LECTIN-LIKE DOMAINS
1258	1c3a	B	31	183	1.4e-30	0.03	0.01		FLAVOCETIN-A: ALPHA SUBUNIT; CHAIN: A; FLAVOCETIN-A: BETA SUBUNIT; CHAIN: B	MEMBRANE PROTEIN C-TYPE LECTIN-LIKE DOMAINS

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1258	1dv8	A	31	180	6.4e-28	0.72	0.68		ASIALOGLYCOPROTEIN RECEPTOR 1; CHAIN: A;	SIGNALING PROTEIN HEPATIC LECTIN H1; C-TYPE LECTIN CRD
1258	1c5u	I	52	80	0.0093	-0.69	0.57		INTIMIN; CHAIN: I;	INTIMIN INT190; INTIMIN, ESCHERICHIA COLI, CELL ADHESION, OUTER MEMBRANE 2 PROTEIN, NMR SPECTROSCOPY
1258	1egg	B	29	187	1.6e-29	0.41	0.36		MACROPHAGE MANNOSE RECEPTOR; CHAIN: A, B;	SUGAR BINDING PROTEIN C-TYPE LECTIN, MANNOSE RECEPTOR
1258	1esl		44	213	4.8e-30	0.45	0.89		CELL ADHESION PROTEIN E-SELECTIN (LECTIN AND EGF DOMAINS, RESIDUES 1 - 157) IESL 3 (FORMERLY KNOWN AS ELAM-1) IESL 4	
1258	1esl		45	220	4.8e-30			60.26	CELL ADHESION PROTEIN E-SELECTIN (LECTIN AND EGF DOMAINS, RESIDUES 1 - 157) IESL 3 (FORMERLY KNOWN AS ELAM-1) IESL 4	
1258	1f00	I	52	80	0.0093	-0.19	0.40		INTIMIN; CHAIN: I;	CELL ADHESION IMMUNOGLOBULIN-LIKE FOLD, C-TYPE LECTIN-LIKE FOLD
1258	1htn		12	184	1.3e-23			68.61	TETRANECTIN; CHAIN: NULL;	LECTIN TETRANECTIN, PLASMINOGEN BINDING, KRINGLE 4, ALPHA-HELICAL 2 COILED COIL, C-TYPE LECTIN, CARBOHYDRATE RECOGNITION DOMAIN
1258	1hup		8	183	6.4e-21			50.48	MANNOSE-BINDING PROTEIN; IHUP 4 CHAIN: NULL; IHUP 5	C-TYPE LECTIN ALPHA-HELICAL COILED-COIL IHUP 12
1258	1ixx	A	31	180	4.8e-32	0.21	0.21		COAGULATION FACTORS IX/X-BINDING PROTEIN; CHAIN: A, B, C, D, E, F;	COAGULATION FACTOR BINDING IX/X-BP COAGULATION FACTOR BINDING, C-TYPE LECTIN, GLA-DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER
1258	1ixx	A	34	181	4.8e-32			58.55	COAGULATION FACTORS	COAGULATION FACTOR BINDING

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									IX/X-BINDING PROTEIN; CHAIN: A, B, C, D, E, F;	IX/X-BP COAGULATION FACTOR BINDING, C-TYPE LECTIN, GLA-DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER
1258	1ixx	B	31	183	1.3e-29	0.24	0.45		COAGULATION FACTORS IX/X-BINDING PROTEIN; CHAIN: A, B, C, D, E, F;	COAGULATION FACTOR BINDING IX/X-BP COAGULATION FACTOR BINDING, C-TYPE LECTIN, GLA-DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER
1258	1ixx	B	34	183	1.3e-29			53.06	COAGULATION FACTORS IX/X-BINDING PROTEIN; CHAIN: A, B, C, D, E, F;	COAGULATION FACTOR BINDING IX/X-BP COAGULATION FACTOR BINDING, C-TYPE LECTIN, GLA-DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER
1258	1lit		31	182	1.6e-31	0.51	0.30		LITHOSTATHINE; CHAIN: NULL	PANCREATIC STONE INHIBITOR, PANCREATIC STONE INHIBITOR, LECTIN
1258	1lit		31	183	1.6e-31			71.84	LITHOSTATHINE; CHAIN: NULL	PANCREATIC STONE INHIBITOR, PANCREATIC STONE INHIBITOR, LECTIN
1258	1qdd	A	18	183	1.6e-31			72.35	LITHOSTATHINE; CHAIN: A;	METAL BINDING PROTEIN PANCREATIC STONE PROTEIN, PSP; PANCREATIC STONE INHIBITOR, LITHOSTATHINE
1258	1qdd	A	31	182	1.6e-31	0.65	0.52		LITHOSTATHINE; CHAIN: A;	METAL BINDING PROTEIN PANCREATIC STONE PROTEIN, PSP; PANCREATIC STONE INHIBITOR, LITHOSTATHINE
1258	1rtm	1	3	183	5.1e-19			50.72	LECTIN MANNOSE-BINDING PROTEIN A (CLOSTRIPAIN FRAGMENT) (CL-MBP-A) 1RTM 3 1RTM 96	
1258	1tm3		28	184	1.2e-24			59.80	TETRAECTIN; CHAIN: NULL;	LECTIN TETRAECTIN, PLASMINOGEN BINDING, KRINGLE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										4, C-TYPE LECTIN, 2 CARBOHYDRATE RECOGNITION DOMAIN
1258	2afp	A	29	179	1.6e-27	-0.06	0.54		SEA RAVEN TYPE II ANTIFREEZE PROTEIN; CHAIN: A;	ANTIFREEZE PROTEIN RECOMBINANT SEA RAVEN PROTEIN, SOLUTION BACKBONE FOLD, C-2 TYPE LECTIN, ANTIFREEZE PROTEIN
1259	1dap	A	1	33	4.8e-05	-0.51	0.13		DIAMINOPIMELIC ACID DEHYDROGENASE; CHAIN: A, B;	OXIDOREDUCTASE DAPDH; NADP, DEHYDROGENASE, D-AMINO ACID DEHYDROGENASE, LYSINE 2 BIOSYNTHESIS, ASYMMETRIC DIMER, OXIDOREDUCTASE
1259	3gpd	R	2	336	0			491.59	OXIDOREDUCTASE (NAD\$(A)-ALDEHYDE(D)) D-GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (E.C.1.2.1.12) 3GPD 4	
1259	3gpd	R	3	336	0	0.93	1.00		OXIDOREDUCTASE (NAD\$(A)-ALDEHYDE(D)) D-GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (E.C.1.2.1.12) 3GPD 4	
1263	1a7c	A	82	463	4.8e-91			115.78	PLASMINOGEN ACTIVATOR INHIBITOR TYPE 1; CHAIN: A; PENTAPEPTIDE; CHAIN: B, C	COMPLEX (PROTEASE INHIBITOR/PEPTIDE) PAI-1; SERINE PROTEASE INHIBITOR, PAI-1, CARBOHYDRATE, INHIBITOR 2 COMPLEX, PEPTIDE
1263	1as4	A	88	430	0	0.25	0.96		ANTICHYMYOTRYPIN; CHAIN: A, B;	SERPIN ACT; SERPIN, SERINE PROTEASE INHIBITOR,

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1263	1as4	A	90	438	0			104.85	ANTICHYMOTRYPSIN; CHAIN: A, B;	ANTICHYMOTRYPSIN SERPIN ACT; SERPIN, SERINE PROTEASE INHIBITOR, ANTICHYMOTRYPSIN
1263	1ath	B	101	464	1.3e-96			102.92	HUMAN ANTITHROMBIN-III ANTITHROMBIN III 1ATH 3	
1263	1ath	B	85	464	1.3e-96	0.23	1.00		HUMAN ANTITHROMBIN-III ANTITHROMBIN III 1ATH 3	
1263	1by7	A	86	463	0	0.68	1.00		PLASMINOGEN ACTIVATOR INHIBITOR-2; CHAIN: A;	PROTEIN BINDING PAI-2; SERPIN, PROTEIN BINDING
1263	1by7	A	86	463	0			101.02	PLASMINOGEN ACTIVATOR INHIBITOR-2; CHAIN: A;	PROTEIN BINDING PROTEIN BINDING
1263	1d5s	B	433	463	1.3e-09	-0.75	0.04		PI-ARG ANTITRYPSIN; CHAIN: A; PI-ARG ANTITRYPSIN; CHAIN: B;	HYDROLASE INHIBITOR SERPIN FOLD, RCL CLEAVAGE, A BETA SHEET POLYMERISATION
1263	1db2	A	83	463	3.2e-94			120.11	PLASMINOGEN ACTIVATOR INHIBITOR-1; CHAIN: A, B;	HYDROLASE INHIBITOR NATIVE SERPIN, HYDROLASE INHIBITOR
1263	1ezx	A	86	432	0	0.23	0.80		ALPHA-1-ANTITRYPSIN; CHAIN: A; ALPHA-1- ANTITRYPSIN; CHAIN: B; TRYPSIN; CHAIN: C;	HYDROLASE/HYDROLASE INHIBITOR PROTEASE-INHIBITOR COMPLEX, SERPIN, ALPHA-1- ANTITRYPSIN, 2 TRYPSIN
1263	1hle	A	85	426	3.2e-98	0.38	1.00		HYDROLASE INHIBITOR(SERINE PROTEINASE) HORSE LEUKOCYTE ELASTASE INHIBITOR (HLEI) 1HLE 3	
1263	1hle	A	85	432	3.2e-98			84.90	HYDROLASE INHIBITOR(SERINE PROTEINASE) HORSE LEUKOCYTE ELASTASE INHIBITOR (HLEI) 1HLE 3	
1263	1ova	A	80	463	0			126.84	SERPIN OVALBUMIN (EGG ALBUMIN) 1OVA 3	
1263	1ova	A	87	463	0	0.62	1.00		SERPIN OVALBUMIN (EGG)	

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1263	1qlp	A	86	463	0	0.49	1.00		ALBUMIN) IOVA 3 ALPHA-1-ANTITRYPSIN; CHAIN: A;	SERINE PROTEASE INHIBITOR ALPHA-1-PROTEINASE INHIBITOR, ALPHA-1-ANTIPROTEINASE; SERINE PROTEASE INHIBITOR, SERPIN, GLYCOPROTEIN, SIGNAL, 2 POLYMORPHISM, EMPHYSEMA, DISEASE MUTATION, ACUTE PHASE
1263	1qlp	A	88	466	0			146.76	ALPHA-1-ANTITRYPSIN; CHAIN: A;	SERINE PROTEASE INHIBITOR ALPHA-1-PROTEINASE INHIBITOR, ALPHA-1-ANTIPROTEINASE; SERINE PROTEASE INHIBITOR, SERPIN, GLYCOPROTEIN, SIGNAL, 2 POLYMORPHISM, EMPHYSEMA, DISEASE MUTATION, ACUTE PHASE
1263	1qmb	B	433	463	4.8e-09	-0.75	0.12		ALPHA-1-ANTITRYPSIN; CHAIN: A, B;	SERINE PROTEASE INHIBITOR ALPHA-1-PROTEINASE INHIBITOR, ALPHA-1-PI; SERPIN, ANTITRYPSIN, POLYMER, CLEAVED
1263	1qmn	A	88	464	0	0.44	1.00		ALPHA-1- ANTICHYMOTRYPSIN; CHAIN: A;	SERPIN AACT SERPIN, SERINE PROTEINASE INHIBITOR, PARTIAL LOOP 2 INSERTION, LOOP-SHEET POLYMERIZATION, EMPHYSEMA, DISEASE 3 MUTATION, ACUTE PHASE PROTEIN, CONFORMATIONAL DISEASE
1263	1sek		80	463	3.2e-85			102.05	SERPIN K; CHAIN: NULL;	SERINE PROTEASE INHIBITOR SERINE PROTEASE INHIBITOR, SERPIN, PROTEASE
1263	2ant	I	47	466	0			139.88	ANTITHROMBIN; CHAIN: L, I;	SERPIN SERPIN, HEPARIN, INHIBITOR
1263	2ant	I	49	464	0	0.48	1.00		ANTITHROMBIN; CHAIN: L, I;	SERPIN SERPIN, HEPARIN,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1263	2ant	L	59	466	0			125.53	ANTITHROMBIN; CHAIN: L, I;	INHIBITOR
1263	2ant	L	81	464	0	0.63	1.00		ANTITHROMBIN; CHAIN: L, I;	SERPIN SERPIN, HEPARIN, INHIBITOR
1264	1aln	A	25	218	6.4e-92	0.93	1.00		B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1264	1aln	A	25	219	1.2e-93			237.20	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1264	1aln	A	26	210	1.2e-93	1.19	1.00		B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1264	1agd	A	25	218	3.2e-92	0.97	1.00		B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1264	1agd	A	25	219	3.2e-92			239.77	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1264	1agd	A	26	210	8.5e-92	0.98	1.00		B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									(GGKKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX
1264	1duz	A	25	218	1.6e-88	1.03	1.00		HLA-A*0201; CHAIN: A, D; BETA-2 MICROGLOBULIN; CHAIN: B, E; HTLV-1 OCTAMERIC TAX PEPTIDE; CHAIN: C, F;	IMMUNE SYSTEM IMMUNOGLOBULIN FOLD
1264	1efx	A	25	218	9.6e-91	1.13	1.00		HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D, E;	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1264	1efx	A	26	210	8.5e-93	1.29	1.00		HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D, E;	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1264	1hoc	A	25	218	1.6e-84			206.63	HISTOCOMPATIBILITY ANTIGEN MURINE CLASS I MAJOR HISTOCOMPATIBILITY COMPLEX CONSISTING 1HOC 3 OF H-2D=B==, B2-MICROGLOBULIN, AND A 9-RESIDUE PEPTIDE 1HOC 4	
1264	1hsa	A	25	218	3.2e-91	0.91	1.00		HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN 1HSA 3 /HLA-B(ASTERISK)2705\$ 1HSA 4	
1264	1hsa	A	25	219	3.2e-91			231.27	HISTOCOMPATIBILITY	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN I HSA 3 /HLA-B(ASTERISK)2705\$ I HSA 4	
1264	lhsb	A	25	218	3.2e-89	1.15	1.00		HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE I HSB 3 ANTIGEN) I HSB 4	
1264	lhsb	A	25	219	3.2e-89			226.78	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE I HSB 3 ANTIGEN) I HSB 4	
1264	lmhe	A	26	219	4.8e-88			209.47	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-E; CHAIN: A, C; BETA-2-MICROGLOBULIN; CHAIN: B, D; PEPTIDE (VMAPRTVLL); CHAIN: P, Q;	MAJOR HISTOCOMPATIBILITY COMPLEX MHC NONCLASSICAL CHAIN, MHC-E, HLA-E, MHC CLASS HLA-E, HLA E, MAJOR HISTOCOMPATIBILITY COMPLEX, MHC, HLA, 2 BETA 2 MICROGLOBULIN, PEPTIDE, LEADER PEPTIDE, 3 NON-CLASSICAL MHC, CLASS IB MHC IMMUNE SYSTEM
1264	lqqd	A	26	218	6.4e-89	1.17	1.00		HISTOCOMPATIBILITY LEUKOCYTE ANTIGEN (HLA)-CW4 CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C;	IMMUNOGLOBULIN (IG)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM
1264	lmc	A	25	199	9.6e-81			257.75	HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									HISTOCOMPATIBILITY ANTIGEN HLA-AW68 ITMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) ITMC 4	
1265	1aln	A	25	212	0	0.82	1.00		B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1265	1aln	A	25	213	0			222.84	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1265	1agd	A	25	212	0	0.93	1.00		B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1265	1agd	A	25	213	0			242.14	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1265	1efx	A	25	212	4.8e-100	0.96	1.00		HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D, E;	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1265	1hsa	A	25	212	1.6e-100	1.04	1.00		HISTOCOMPATIBILITY	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1265	1hsa	A	25	213	1.6e-100				ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN 1HSA 3 /HLA-B(ASTERISK)2705\$ 1HSA 4 HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN 1HSA 3 /HLA-B(ASTERISK)2705\$ 1HSA 4	
1265	1qqd	A	26	212	1.3e-98	0.83	1.00		HISTOCOMPATIBILITY LEUKOCYTE ANTIGEN (HLA)-CW4 CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C;	IMMUNE SYSTEM IMMUNOGLOBULIN (IG)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM
1265	1tmc	A	25	199	3.2e-93	1.00	1.00		HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-AW68 1TMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) 1TMC 4	
1265	1tmc	A	25	199	3.2e-93			245.23	HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-AW68 1TMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) 1TMC 4	
1266	1aln	A	22	210	4.8e-97	0.88	1.00		B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1266	1aln	A	22	210	4.8e-97			202.13	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1266	lagd	A	22	210	1.1e-97	0.92	1.00		B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1266	lagd	A	22	210	1.1e-97			212.14	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1266	lduz	A	22	208	4.8e-95	0.88	1.00		HLA-A*0201; CHAIN: A, D; BETA-2 MICROGLOBULIN; CHAIN: B, E; HTLV-1 OCTAMERIC TAX PEPTIDE; CHAIN: C, F;	IMMUNE SYSTEM IMMUNOGLOBULIN FOLD
1266	lefx	A	22	210	3.2e-96	1.08	1.00		HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D, E;	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1266	lhas	A	22	210	3.2e-96	0.89	1.00		HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN I HSA 3 /HLA-	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1266	1hsa	A	22	210	3.2e-96			195.27	B(ASTERISK)2705\$ IHS A 4 HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN IHS A 3 /HLA- B(ASTERISK)2705\$ IHS A 4	
1266	1hsb	A	22	208	4.8e-96	0.87	1.00		HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE IHSB 3 ANTIGEN) IHSB 4	
1266	1hsb	A	22	210	4.8e-96			189.34	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE IHSB 3 ANTIGEN) IHSB 4	
1266	1qgd	A	23	210	3.2e-94	0.89	1.00		HISTOCOMPATIBILITY LEUCOCYTE ANTIGEN (HLA)- CW4 CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C;	IMMUNE SYSTEM IMMUNOGLOBULIN (IG)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM
1266	1tmc	A	22	197	4.8e-90	0.98	1.00		HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-AW68 1TMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) 1TMC 4	
1266	1tmc	A	22	197	4.8e-90			228.77	HISTOCOMPATIBILITY ANTIGEN TRUNCATED	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-A*W68 ITMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) ITMC 4	
1267	1a1n	A	25	214	6.4e-100	1.01	1.00		B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1267	1a1n	A	25	214	6.4e-100			206.29	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1267	1agd	A	25	214	1.6e-100	0.95	1.00		B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1267	1agd	A	25	214	1.6e-100			193.54	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1267	1duz	A	25	214	3.2e-97	0.96	1.00		HLA-A*0201; CHAIN: A, D; BETA-2 MICROGLOBULIN; CHAIN: B, E; HTLV-1 OCTAMERIC TAX PEPTIDE; CHAIN: C, F;	IMMUNE SYSTEM IMMUNOGLOBULIN FOLD
1267	1efx	A	25	214	1.6e-98	0.91	1.00		HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2-	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D, E;	IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1267	1hsa	A	25	214	1.6e-99	1.02	1.00		HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN 1HSA 3 /HLA-B(ASTERISK)2705\$ 1HSA 4	
1267	1hsa	A	25	214	1.6e-99			198.64	HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN 1HSA 3 /HLA-B(ASTERISK)2705\$ 1HSA 4	
1267	1hsb	A	25	214	1.1e-98	0.98	1.00		HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE 1HSB 3 ANTIGEN) 1HSB 4	
1267	1hsb	A	25	214	1.1e-98			190.28	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE 1HSB 3 ANTIGEN) 1HSB 4	
1267	1qqd	A	26	214	4.8e-97	0.95	1.00		HISTOCOMPATIBILITY LEUCOCYTE ANTIGEN (HLA)-CW4 CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C;	IMMUNE SYSTEM IMMUNOGLOBULIN (IG)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM
1267	1tmc	A	25	200	6.4e-91	0.91	1.00		HISTOCOMPATIBILITY	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-AW68 ITMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) ITMC 4	
1267	1tmc	A	25	200	6.4e-91			227.42	HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-AW68 ITMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) ITMC 4	
1268	1a1n	A	25	301	0	0.83	1.00		B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1268	1a1n	A	25	301	0			381.69	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1268	lagd	A	25	301	0	0.79	1.00		B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1268	lagd	A	25	301	0			382.18	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									(GGKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX
1268	1dn2	A	224	314	0.00034	-0.28	0.00		IMMUNOGLOBULIN LAMBDA HEAVY CHAIN; CHAIN: A; B; ENGINEERED PEPTIDE; CHAIN: E, F;	IMMUNE SYSTEM FC IGG PHAGE DISPLAY PEPTIDE
1268	1duz	A	25	300	0	0.83	1.00		HLA-A*0201; CHAIN: A; D; BETA-2 MICROGLOBULIN; CHAIN: B; E; HTLV-1 OCTAMERIC TAX PEPTIDE; CHAIN: C, F;	IMMUNE SYSTEM IMMUNOGLOBULIN FOLD
1268	1efx	A	25	303	0	0.83	1.00		HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D, E;	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1268	1hsa	A	25	301	0	0.80	1.00		HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN 1HSA 3 /HLA-B(ASTERISK)2705\$ 1HSA 4	
1268	1hsa	A	25	301	0			381.68	HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN 1HSA 3 /HLA-B(ASTERISK)2705\$ 1HSA 4	
1268	1hsb	A	25	295	0	0.82	1.00		HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE 1HSB 3 ANTIGEN) 1HSB 4	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1268	1hsb	A	25	295	0			416.11	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE IHSB 3 ANTIGEN) IHSB 4	
1268	1igt	B	224	308	1.6e-05	0.26	0.71		IGG2A INTACT ANTIBODY - MAB231; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN V REGION C REGION; IMMUNOGLOBULIN
1268	1mco	H	189	310	1.7e-05	0.09	0.23		IMMUNOGLOBULIN IMMUNOGLOBULIN G1 (IGG1) (MCG) WITH A HINGE DELETION IMCO 3	
1268	1mco	H	220	314	6.8e-06	0.30	0.48		IMMUNOGLOBULIN IMMUNOGLOBULIN G1 (IGG1) (MCG) WITH A HINGE DELETION IMCO 3	
1268	1qgd	A	26	299	0	0.63	1.00		HISTOCOMPATIBILITY LEUKOCYTE ANTIGEN (HLA)-CW4 CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C;	IMMUNE SYSTEM IMMUNOGLOBULIN (IG)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM
1269	1aln	A	25	285	0	0.88	1.00		B*3501; CHAIN: A, B; PEPTIDE VPLRPMY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC; HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1269	1aln	A	25	288	0			279.39	B*3501; CHAIN: A, B; PEPTIDE VPLRPMY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1269	1agd	A	25	285	0	0.87	1.00		B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKKYL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1269	1agd	A	25	288	0			278.31	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKKYL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1269	1duz	A	25	285	0	0.93	1.00		HLA-A*0201; CHAIN: A, D; BETA-2 MICROGLOBULIN; CHAIN: B, E; HTLV-1 OCTAMERIC TAX PEPTIDE; CHAIN: C, F;	IMMUNE SYSTEM IMMUNOGLOBULIN FOLD
1269	1efx	A	25	285	0	0.94	1.00		HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D, E;	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1269	1hsa	A	25	285	0	0.93	1.00		HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN 1HSA 3 /HLA-B(ASTERISK)2705\$ 1HSA 4	
1269	1hsa	A	25	288	0			284.65	HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN 1HSA 3 /HLA-B(ASTERISK)2705\$ 1HSA 4	
1269	1hsb	A	25	285	0	0.83	1.00		HISTOCOMPATIBILITY ANTIGEN CLASS I	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE IHSB 3 ANTIGEN) IHSB 4	
1269	1hsb	A	25	288	0			302.23	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE IHSB 3 ANTIGEN) IHSB 4	
1269	1mhe	A	26	285	0	0.70	1.00		HLA CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-E; CHAIN: A, C; BETA-2-MICROGLOBULIN; CHAIN: B, D; PEPTIDE (VMAPRTVLL); CHAIN: P, Q;	MAJOR HISTOCOMPATIBILITY COMPLEX MHC NONCLASSICAL CHAIN, MHC-E, HLA-E, MHC CLASS HLA-E, HLA E, MAJOR HISTOCOMPATIBILITY COMPLEX, MHC, HLA, 2 BETA 2 MICROGLOBULIN, PEPTIDE, LEADER PEPTIDE, 3 NON-CLASSICAL MHC, CLASS IB MHC
1269	1mhe	A	26	288	0			253.44	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-E; CHAIN: A, C; BETA-2-MICROGLOBULIN; CHAIN: B, D; PEPTIDE (VMAPRTVLL); CHAIN: P, Q;	MAJOR HISTOCOMPATIBILITY COMPLEX MHC NONCLASSICAL CHAIN, MHC-E, HLA-E, MHC CLASS HLA-E, HLA E, MAJOR HISTOCOMPATIBILITY COMPLEX, MHC, HLA, 2 BETA 2 MICROGLOBULIN, PEPTIDE, LEADER PEPTIDE, 3 NON-CLASSICAL MHC, CLASS IB MHC
1269	1qqd	A	26	285	0	0.86	1.00		HISTOCOMPATIBILITY LEUCOCYTE ANTIGEN (HLA)-CW4 CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C;	IMMUNE SYSTEM IMMUNOGLOBULIN (IG)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1269	1tmc	A	25	200	8e-88	0.97	1.00		HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-AW68 ITMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) ITMC 4	
1269	1tmc	A	25	200	8e-88			257.46	HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-AW68 ITMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) ITMC 4	
1271	1aln	A	25	218	1.4e-94	0.95	1.00		B*3501; CHAIN: A; B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1271	1aln	A	25	219	5.1e-96			239.16	B*3501; CHAIN: A; B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1271	1aln	A	26	210	5.1e-96	1.03	1.00		B*3501; CHAIN: A; B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1271	1agd	A	25	218	3.2e-95	1.03	1.00		B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									HIV-1 GAG PEPTIDE (GGKKYKL - INDEX PEPTIDE); CHAIN: C;	MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1271	1agd	A	25	219	3.2e-95			243.91	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1271	1duz	A	25	218	3.2e-91	0.93	1.00		HLA-A*0201; CHAIN: A; D; BETA-2 MICROGLOBULIN; CHAIN: B; E; HTLV-1 OCTAMERIC TAX PEPTIDE; CHAIN: C, F;	IMMUNE SYSTEM IMMUNOGLOBULIN FOLD
1271	1efx	A	25	218	1.6e-93	0.95	1.00		HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D, E;	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1271	1efx	A	26	210	1e-95	1.16	1.00		HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D, E;	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1271	1hsa	A	25	218	4.8e-94	0.99	1.00		HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN 1HSA 3 /HLA-B(ASTERISK)2705\$ 1HSA 4	
1271	1hsa	A	25	219	4.8e-94			235.85	HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									HISTOCOMPATIBILITY ANTIGEN I HSA 3 /HLA-B(ASTERISK)2705\$ I HSA 4	
1271	1hsb	A	25	218	4.8e-92	1.11	1.00		HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE I HSB 3 ANTIGEN) I HSB 4	
1271	1hsb	A	25	219	4.8e-92			238.52	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE I HSB 3 ANTIGEN) I HSB 4	
1271	1mhc	A	26	218	1.6e-92	0.94	1.00		HLA CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-E; CHAIN: A, C; BETA-2-MICROGLOBULIN; CHAIN: B, D; PEPTIDE (VMAPRTVLL); CHAIN: P, Q;	MAJOR HISTOCOMPATIBILITY COMPLEX MHC NONCLASSICAL CHAIN, MHC-E, HLA-E, MHC CLASS HLA-E, HLA E, MAJOR HISTOCOMPATIBILITY COMPLEX, MHC, HLA, 2 BETA 2 MICROGLOBULIN, PEPTIDE, LEADER PEPTIDE, 3 NON- CLASSICAL MHC, CLASS IB MHC
1271	1mhc	A	26	219	1.6e-92			218.16	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-E; CHAIN: A, C; BETA-2-MICROGLOBULIN; CHAIN: B, D; PEPTIDE (VMAPRTVLL); CHAIN: P, Q;	MAJOR HISTOCOMPATIBILITY COMPLEX MHC NONCLASSICAL CHAIN, MHC-E, HLA-E, MHC CLASS HLA-E, HLA E, MAJOR HISTOCOMPATIBILITY COMPLEX, MHC, HLA, 2 BETA 2 MICROGLOBULIN, PEPTIDE, LEADER PEPTIDE, 3 NON- CLASSICAL MHC, CLASS IB MHC
1271	1gqd	A	26	218	1.6e-92	0.95	1.00		HISTOCOMPATIBILITY	IMMUNE SYSTEM

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									LEUKOCYTE ANTIGEN (HLA)-CW4 CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C;	IMMUNOGLOBULIN (IG)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM
1271	1tmc	A	25	199	1.4e-83			267.94	HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-AW68 1TMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) 1TMC 4	
1272	1aln	A	25	213	8e-91	0.92	1.00		B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1272	1aln	A	25	213	8e-91			150.68	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1272	lagd	A	25	213	3.2e-91	0.79	1.00		B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1272	lagd	A	25	213	3.2e-91			152.02	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1272	1duz	A	25	213	6.4e-90	0.75	1.00		HLA-A*0201; CHAIN: A, D; BETA-2 MICROGLOBULIN; CHAIN: B, E; HTLV-1 OCTAMERIC TAX PEPTIDE; CHAIN: C, F;	IMMUNE SYSTEM IMMUNOGLOBULIN FOLD
1272	1efx	A	25	213	6.4e-91	0.89	1.00		HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2- MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D, E;	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1272	1hsa	A	25	213	1.6e-90	0.92	1.00		HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN I HSA 3 /HLA- B(ASTERISK)2705\$ I HSA 4	
1272	1hsa	A	25	213	1.6e-90			151.46	HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN I HSA 3 /HLA- B(ASTERISK)2705\$ I HSA 4	
1272	1hsb	A	25	213	3.2e-91	0.87	1.00		HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE I HSB 3 ANTIGEN) I HSB 4	
1272	1hsb	A	25	213	3.2e-91			178.43	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE I HSB 3 ANTIGEN) I HSB 4	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1272	1mhe	A	26	213	4.8e-87	0.92	1.00		HLA CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-E; CHAIN: A, C; BETA-2-MICROGLOBULIN; CHAIN: B, D; PEPTIDE (VMAPRTVLL); CHAIN: P, Q;	MAJOR HISTOCOMPATIBILITY COMPLEX MHC NONCLASSICAL CHAIN, MHC-E, HLA-E, MHC CLASS HLA-E, HLA E, MAJOR HISTOCOMPATIBILITY COMPLEX, MHC, HLA, 2 BETA 2 MICROGLOBULIN, PEPTIDE, LEADER PEPTIDE, 3 NON-CLASSICAL MHC, CLASS IB MHC
1272	1mhe	A	26	213	4.8e-87			144.34	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-E; CHAIN: A, C; BETA-2-MICROGLOBULIN; CHAIN: B, D; PEPTIDE (VMAPRTVLL); CHAIN: P, Q;	MAJOR HISTOCOMPATIBILITY COMPLEX MHC NONCLASSICAL CHAIN, MHC-E, HLA-E, MHC CLASS HLA-E, HLA E, MAJOR HISTOCOMPATIBILITY COMPLEX, MHC, HLA, 2 BETA 2 MICROGLOBULIN, PEPTIDE, LEADER PEPTIDE, 3 NON-CLASSICAL MHC, CLASS IB MHC
1272	1qqd	A	26	213	8e-89	0.67	1.00		HISTOCOMPATIBILITY LEUKOCYTE ANTIGEN (HLA)-CW4 CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C;	IMMUNE SYSTEM IMMUNOGLOBULIN (IG)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM
1272	1tmc	A	25	201	9.6e-87	0.83	1.00		HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-AW68 ITMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) ITMC 4	
1272	1tmc	A	25	205	9.6e-87			215.19	HISTOCOMPATIBILITY ANTIGEN TRUNCATED	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-AW68 1TMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) 1TMC 4	
1273	1aln	A	25	205	6.4e-97	0.98	1.00		B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1273	1aln	A	25	219	6.4e-97			221.84	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1273	1agd	A	25	205	3.2e-97	1.14	1.00		B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1273	1agd	A	25	219	3.2e-97			223.96	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1273	1duz	A	25	205	1.1e-95	1.27	1.00		HLA-A*0201; CHAIN: A; D; BETA-2 MICROGLOBULIN; CHAIN: B; E; HTLV-1 OCTAMERIC TAX PEPTIDE; CHAIN: C, F;	IMMUNE SYSTEM IMMUNOGLOBULIN FOLD
1273	1efx	A	25	205	4.8e-97	1.17	1.00		HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2-	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D, E;	IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1273	1hsa	A	25	205	1.6e-96	1.12	1.00		HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN 1HSA 3 /HLA-B(ASTERISK)2705\$ 1HSA 4	
1273	1hsa	A	25	219	1.6e-96			222.04	HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN 1HSA 3 /HLA-B(ASTERISK)2705\$ 1HSA 4	
1273	1hsb	A	25	205	1.6e-97	1.03	1.00		HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE 1HSB 3 (ANTIGEN) 1HSB 4	
1273	1hsb	A	25	218	1.6e-97			245.70	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE 1HSB 3 (ANTIGEN) 1HSB 4	
1273	1qqd	A	26	205	1.1e-95	1.07	1.00		HISTOCOMPATIBILITY LEUCOCYTE ANTIGEN (HLA)-CW4 CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C;	IMMUNE SYSTEM IMMUNOGLOBULIN (IG)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM
1273	1tmc	A	25	199	1.6e-93	1.25	1.00		HISTOCOMPATIBILITY	

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-AW68 ITMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) ITMC 4	
1273	1tmc	A	25	199	1.6e-93			273.81	HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-AW68 ITMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) ITMC 4	
1274	1buo	A	1	126	1.6e-22	0.30	1.00		PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;	GENE REGULATION POZ DOMAIN; PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2 REPRESSOR, ZINC-FINGER PROTEIN, X-RAY CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC LEUKEMIA, GENE REGULATION
1274	1buo	A	5	128	3.4e-28	0.41	0.99		PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;	GENE REGULATION POZ DOMAIN; PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2 REPRESSOR, ZINC-FINGER PROTEIN, X-RAY CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC LEUKEMIA, GENE REGULATION
1274	1gof		291	458	1.1e-11	0.05	0.17		OXIDOREDUCTASE(OXYGEN(A)) GALACTOSE OXIDASE	

SEQ ID NO;	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1274	lgof		383	495	1.6e-08	0.27	0.13		(E.C.1.1.3.9) (PH 4.5) IGOF 3 OXIDOREDUCTASE(OXYGEN(A)) GALACTOSE OXIDASE (E.C.1.1.3.9) (PH 4.5) IGOF 3	
1275	lcun	A	170	385	6.8e-09			65.74	ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1275	lquu	A	180	415	3.4e-12			59.43	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
1275	lsig		130	416	5.1e-05			76.16	RNA POLYMERASE PRIMARY SIGMA FACTOR; CHAIN: NULL;	TRANSCRIPTION REGULATION SIGMA70; RNA POLYMERASE SIGMA FACTOR, TRANSCRIPTION REGULATION
1276	labr	B	413	552	1.4e-09	0.45	0.40		COMPLEX (GLYCOSIDASE/CARBOHYDRATE) ABRIN-A COMPLEXED WITH TWO SUGAR CHAINS I ABR 3	
1276	lee7	B	441	552	1.2e-15	0.16	0.21		RIBOSOME-INACTIVATING PROTEIN TYPE II; CHAIN: A; RIBOSOME-INACTIVATING PROTEIN TYPE II; CHAIN: B	RIBOSOME RIBOSOME-INACTIVATING PROTEIN TYPE II
1276	lee7	B	450	543	0.00011	-0.25	0.13		RIBOSOME-INACTIVATING PROTEIN TYPE II; CHAIN: A; RIBOSOME-INACTIVATING PROTEIN TYPE II; CHAIN: B	RIBOSOME RIBOSOME-INACTIVATING PROTEIN TYPE II
1276	lqgq	A	123	345	6.4e-22	0.09	0.28		SPORE COAT POLYSACCHARIDE BIOSYNTHESIS PROTEIN	TRANSFERASE GLYCOSYLTRANSFERASE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1276	1xyf	A	441	543	1.6e-16	-0.02	0.66		CHAIN: A; ENDO-1,4-BETA-XYLANASE; CHAIN: A, B;	HYDROLASE XYLAN DEGRADATION
1276	2aai	B	441	543	1.3e-07	-0.31	0.03		GLYCOSIDASE RICIN (E.C.3.2.2.22) 2AAI 3	
1279	2ak3	A	1	38	1.3e-16	-0.87	0.98		TRANSFERASE (PHOSPHOTRANSFERASE) ADENYLATE KINASE ISOENZYME-3 (GTP: AMP PHOSPHOTRANSFERASE) 2AK3 3 (E.C.2.7.4.10) 2AK3 4	
1280	12e8	H	59	253	1.3e-38	0.01	0.21		2E8 (IGG1=KAPPA=) ANTIBODY; CHAIN: L, H, M, P;	IMMUNOGLOBULIN IMMUNOGLOBULIN
1280	1a0q	H	50	254	6.4e-37			61.67	29G11 FAB; CHAIN: L, H;	CATALYTIC ANTIBODY CATALYTIC ANTIBODY, ESTERASE
1280	1a0q	H	59	253	6.4e-37	-0.31	0.27		29G11 FAB; CHAIN: L, H;	CATALYTIC ANTIBODY CATALYTIC ANTIBODY, ESTERASE
1280	1a3r	H	50	256	1.3e-36			60.58	IGG2A; CHAIN: L, H; HUMAN RHINOVIRUS CAPSID PROTEIN VP2; CHAIN: P;	COMPLEX (IMMUNOGLOBULIN/VIRAL PEPTIDE) ANTIBODY 8F5; IMMUNOGLOBULIN, ANTIBODY, RHINOVIRUS, NEUTRALIZATION, 2 CONTINUOUS EPTOPE, COMPLEX (IMMUNOGLOBULIN/VIRAL PEPTIDE)
1280	1a4j	L	51	252	9.6e-37	-0.11	0.17		IMMUNOGLOBULIN, DIELS ALDER CATALYTIC ANTIBODY; CHAIN: L, H, A, B;	IMMUNOGLOBULIN IMMUNOGLOBULIN, ANTIBODY, CATALYTIC ANTIBODY, DIELS ALDER, 2 GERMLINE
1280	1a5f	H	48	256	3.2e-35			61.06	MONOCLONAL ANTI-E-SELECTIN 7A9 ANTIBODY; CHAIN: L, H;	IMMUNOGLOBULIN, FAB, ANTIBODY, ANTI-E-SELECTIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1280	1adq	L	50	255	1.1e-37	-0.04	0.00		IGG4 REA; CHAIN: A; RF-AN IGM/LAMBDA; CHAIN: H, L;	COMPLEX (IMMUNOGLOBULIN/AUTOANTIGEN) COMPLEX (IMMUNOGLOBULIN/AUTOANTIGEN), RHEUMATOID FACTOR 2 AUTO-ANTIBODY COMPLEX
1280	1afv	H	52	253	4.8e-37	0.08	0.58		HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 CAPSID CHAIN: A, B; ANTIBODY FAB25.3 FRAGMENT; CHAIN: H, K, L, M;	COMPLEX (VIRAL CAPSID/IMMUNOGLOBULIN) HIV-1 CA, HIV CA, HIV P24, P24; FAB, FAB LIGHT CHAIN, FAB HEAVY CHAIN COMPLEX (VIRAL CAPSID/IMMUNOGLOBULIN), HIV, CAPSID PROTEIN, 2 P24
1280	1axt	H	51	256	4.8e-33			56.82	IMMUNOGLOBULIN IGG2A; CHAIN: L, H;	IMMUNOGLOBULIN ANTIBODY FAB, CATALYST, ALDOLASE REACTION
1280	1b2w	L	51	258	8e-39	0.04	-0.07		ANTIBODY (LIGHT CHAIN); CHAIN: L; ANTIBODY (HEAVY CHAIN); CHAIN: H;	IMMUNE SYSTEM IMMUNOGLOBULIN; IMMUNOGLOBULIN ANTIBODY ENGINEERING, HUMANIZED AND CHIMERIC ANTIBODY, FAB, 2 X-RAY STRUCTURE, THREE-DIMENSIONAL STRUCTURE, GAMMA-3 INTERFERON, IMMUNE SYSTEM
1280	1b4j	L	51	258	1.4e-37	0.00	0.09		ANTIBODY; CHAIN: L, H;	ANTIBODY ENGINEERING ANTIBODY ENGINEERING, HUMANIZED AND CHIMERIC ANTIBODIES, 2 FAB, X-RAY STRUCTURES, GAMMA-INTERFERON
1280	1b6d	A	51	252	4.8e-37	-0.12	0.13		IMMUNOGLOBULIN; CHAIN: A, B;	IMMUNOGLOBULIN IMMUNOGLOBULIN, KAPPA LIGHT-

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1280	1bjl	L	51	252	8e-38	0.09	-0.09		FAB FRAGMENT; CHAIN: L, H, J, K; VASCULAR ENDOTHELIAL GROWTH FACTOR; CHAIN: V, W;	CHAIN DIMER HEADER COMPLEX (ANTIBODY/ANTIGEN) FAB-12; VEGF; COMPLEX (ANTIBODY/ANTIGEN), ANGIOGENIC FACTOR
1280	1bln	A	47	252	4.8e-35			57.09	MONOCLONAL ANTIBODY MRK-16 (LIGHT CHAIN); CHAIN: A, C; MONOCLONAL ANTIBODY MRK-16 (HEAVY CHAIN); CHAIN: B, D;	IMMUNE SYSTEM IMMUNOGLOBULIN, IMMUNE SYSTEM
1280	1bm3	H	51	258	1.6e-34			57.73	IMMUNOGLOBULIN OPG2 FAB, CONSTANT DOMAIN; CHAIN: L; IMMUNOGLOBULIN OPG2 FAB, VARIABLE DOMAIN; CHAIN: H;	IMMUNE SYSTEM IMMUNOGLOBULIN
1280	1bql	H	50	255	3.2e-36			59.53	COMPLEX (ANTIBODY/ANTIGEN) HYHEL-5 FAB COMPLEXED WITH BOBWHITE QUAIL LYSOZYME IBQL 3 IBQL 95	
1280	1bz7	B	51	250	1.6e-26			57.49	ANTIBODY R24 (LIGHT CHAIN); CHAIN: A; ANTIBODY R24 (HEAVY CHAIN); CHAIN: B;	IMMUNE SYSTEM ANTIBODY (FAB FRAGMENT), IMMUNE SYSTEM
1280	1ce1	L	51	252	9.6e-37	0.11	-0.03		CAMPATH-1H:LIGHT CHAIN; CHAIN: L; CAMPATH-1H:HEAVY CHAIN; CHAIN: H; PEPTIDE ANTIGEN; CHAIN: P;	ANTIBODY THERAPEUTIC, ANTIBODY, CD52
1280	1cr9	H	59	255	8e-39	-0.12	0.60		FAB ANTIBODY LIGHT CHAIN; CHAIN: L; FAB ANTIBODY HEAVY CHAIN; CHAIN: H;	IMMUNE SYSTEM ANTI-PRION FAB 3F4; ANTI-PRION FAB 3F4 ANTI-PRION ANTIBODY, FAB 3F4
1280	1fbi	H	48	255	1.6e-36			56.80	COMPLEX (ANTIBODY/ANTIGEN) FAB FRAGMENT OF THE	

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1280	1flr	H	51	256	3.2e-33			56.39	MONOCLONAL ANTIBODY F9.13.7 (IGG1) IFBI 3 COMPLEXED WITH LYSOZYME (E.C.3.2.1.17) IFBI 4	IMMUNOGLOBULIN
1280	1fvd	A	51	258	1.4e-37	0.11	-0.12		4-4-20 (IG*G2A=KAPPA=) FAB FRAGMENT; 1FLR 5 CHAIN: L, H; 1FLR 6	
1280	1fvd	B	51	258	6.4e-32			57.20	IMMUNOGLOBULIN FAB FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 4 IFVD 3	
1280	1hyx	L	47	255	1.3e-34			57.33	IMMUNOGLOBULIN 6D9; CHAIN: L, H;	CATALYTIC ANTIBODY CATALYTIC ANTIBODY 6D9 CATALYTIC ANTIBODY, ESTER HYDROLYSIS, ESTEROLYTIC, FAB, 2 IMMUNOGLOBULIN
1280	liai	H	48	254	4.8e-33			60.65	IDIOTYPIC FAB 730.1.4 (IGG1) OF VIRUS 1IAI 5 CHAIN: L, H; 1IAI 7 ANTI-IDIOTYPIC FAB 409.5.3 (IGG2A); 1IAI 9 CHAIN: M, I 1IAI 10	COMPLEX (IMMUNOGLOBULIN IGG1/IGG2A)
1280	ligc	H	51	258	1.6e-32			57.26	COMPLEX (ANTIBODY/BINDING PROTEIN) IGG1 FAB FRAGMENT COMPLEXED WITH PROTEIN G (DOMAIN IIGC 5 PROTEIN G, STREPTOCOCCUS IIGC 15	
1280	ligf	L	47	258	8e-35			58.26	IMMUNOGLOBULIN IGG1 FAB' FRAGMENT (B1312) IIGF 3	

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1280	ligy	B	59	253	1.6e-36	0.02	0.37		IGG1 INTACT ANTIBODY MAB61.1.3; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN, V REGION, C REGION, HINGE REGION
1280	lkel	H	51	255	6.4e-34			57.31	28B4 FAB; CHAIN: L, H;	CATALYTIC ANTIBODY SULFIDE OXIDATION, MONOOXYGENASE, OXYGENATION, FAB, 2 IMMUNOGLOBULIN, CATALYTIC ANTIBODY
1280	lmlb	B	48	258	8e-36			56.48	IMMUNOGLOBULIN FAB D44.1 (IGG1,KAPPA) (BALB/C MOUSE, MONOCLONAL ANTIBODY) 1MLB 5	
1280	lnct		178	254	0.0015	0.08	0.35		TITIN; CHAIN: NULL;	MUSCLE PROTEIN CONNECTIN, NEXTM5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN
1280	lngp	H	51	253	6.4e-37	-0.09	0.22		NIG9 (IGG1=LAMBDA=); CHAIN: L, H;	IMMUNOGLOBULIN IMMUNOGLOBULIN,
1280	lsm3	H	51	256	1.6e-36			58.83	SM3 ANTIBODY; CHAIN: L, H; PEPTIDE EPITOPE; CHAIN: P;	COMPLEX (ANTIBODY/PEPTIDE EPITOPE) ANTIBODY, PEPTIDE ANTIGEN, ANTITUMOR ANTIBODY, 2 COMPLEX (ANTIBODY/PEPTIDE EPITOPE)
1280	lsm3	H	59	253	1.6e-36	-0.09	0.41		SM3 ANTIBODY; CHAIN: L, H; PEPTIDE EPITOPE; CHAIN: P;	COMPLEX (ANTIBODY/PEPTIDE EPITOPE) ANTIBODY, PEPTIDE ANTIGEN, ANTITUMOR ANTIBODY, 2 COMPLEX (ANTIBODY/PEPTIDE EPITOPE)
1280	lsm3	L	50	252	3.2e-30			56.66	SM3 ANTIBODY; CHAIN: L, H; PEPTIDE EPITOPE; CHAIN: P;	COMPLEX (ANTIBODY/PEPTIDE EPITOPE) ANTIBODY, PEPTIDE ANTIGEN, ANTITUMOR ANTIBODY,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1280	1tet	H	48	256	6.4e-36			57.32	IMMUNOGLOBULIN IGG1 MONOCLONAL FAB FRAGMENT (TE33) COMPLEX WITH CHOLERA 1TET 3 TOXIN PEPTIDE 3 (CTP3) 1TET 4	2 COMPLEX (ANTIBODY/PEPTIDE EPTOPE)
1280	1tnm		178	254	0.0051	-0.05	0.05		MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) 1TNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) 1TNM 4 1TNM 58	
1280	1wej	H	59	253	3.2e-37	0.55	0.70		E8 ANTIBODY; CHAIN: L, H; CYTOCHROME C; CHAIN: F;	COMPLEX (ANTIBODY/ELECTRON TRANSPORT) FAB E8; CYT C, ANTIGEN; IMMUNOGLOBULIN, IGG1 KAPPA, FAB FRAGMENT, HORSE 2 CYTOCHROME C, COMPLEX (ANTIBODY/ELECTRON TRANSPORT)
1280	1wvc	A	164	254	0.0051	-0.18	0.01		NT-3 GROWTH FACTOR RECEPTOR TRKC; CHAIN: A;	TRANSFERASE TRK RECEPTOR, RECEPTOR TYROSINE KINASE, 3D-DOMAIN SWAPPING, 2 TRANSFERASE
1280	25c8	H	48	254	1.1e-37			57.06	IGG 5C8; CHAIN: L, H;	CATALYTIC ANTIBODY CATALYTIC ANTIBODY, FAB, RING CLOSURE REACTION
1280	25c8	H	59	253	1.1e-37	0.11	0.53		IGG 5C8; CHAIN: L, H;	CATALYTIC ANTIBODY CATALYTIC ANTIBODY, FAB, RING CLOSURE REACTION
1280	2cgr	H	51	254	1.6e-31			57.12	IMMUNOGLOBULIN IGG2B (KAPPA) FAB FRAGMENT COMPLEXED WITH ANTIGEN 2CGR 3 N-(p-CYANOPHENYL)-N'-(DIPHENYLEMETHYL)	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									GUANIDINEACETIC ACID 2CGR 4	
1280	2fgw	L	51	258	1.6e-38	0.00	-0.08		IMMUNOGLOBULIN FAB FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 2FGW 3 ANTIBODY 'H52' (HUH52-OZ FAB) 2FGW 4	
1280	2hmi	C	47	258	4.8e-33			56.78	HIV-1 REVERSE TRANSCRIPTASE; CHAIN: A, B; MONOCLONAL ANTIBODY 28; CHAIN: C, D; DNA; CHAIN: E, F; IMMUNOGLOBULIN	COMPLEX (RT/DNA/FAB) HIV-1 RT; FAB 28; AIDS, HIV-1, RT, POLYMERASE
1280	7fab	H	49	255	3.2e-31			57.01	IMMUNOGLOBULIN FAB' NEW (LAMBDA LIGHT CHAIN) 7FAB 3	
1284	1erk	A	1	46	3.2e-19	-0.83	0.27		CREATINE KINASE; CHAIN: A, B, C, D;	TRANSFERASE TRANSFERASE, CREATINE KINASE
1284	1qh4	A	1	46	4.8e-19	-0.83	0.30		CREATINE KINASE, B CHAIN; CHAIN: A, B, C, D;	TRANSFERASE BB-CK, BRAIN-TYPE CREATINE KINASE; BRAIN-TYPE CREATINE KINASE, CANCER, CELLULAR ENERGY 2 METABOLISM, GUANIDINO KINASE, NEURODEGENERATIVE DISORDERS
1284	1qk1	A	1	46	6.4e-19	-0.83	0.33		CREATINE KINASE, UBIQUITOUS MITOCHONDRIAL; CHAIN: A, B, C, D, E, F, G, H;	TRANSFERASE (CREATINE KINASE) UMTCK, MIA-CK; MITOCHONDRIAL CREATINE KINASE, CANCER, CELLULAR ENERGY 2 METABOLISM, GUANIDINO KINASE, MITOCHONDRIAL PERMEABILITY 3 TRANSITION, OCTAMER STABILITY
1284	2crk	A	1	46	1.4e-19	-0.83	0.19		CREATINE KINASE; CHAIN: A;	TRANSFERASE CREATINE KINASE,

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										TRANSFERASE
1287	1bq0		5	69	1.1e-27	0.89	1.00		DNAJ; CHAIN: NULL;	CHAPERONE HSP40; CHAPERONE, HEAT SHOCK, PROTEIN FOLDING, DNAK
1287	1bq0		5	78	1.1e-27			68.92	DNAJ; CHAIN: NULL;	CHAPERONE HSP40; CHAPERONE, HEAT SHOCK, PROTEIN FOLDING, DNAK
1287	1hdj		10	77	3.4e-30	0.77	1.00		HUMAN HSP40; CHAIN: NULL;	MOLECULAR CHAPERONE HDJ-1; MOLECULAR CHAPERONE
1287	1hdj		5	80	3.4e-30			83.03	HUMAN HSP40; CHAIN: NULL;	MOLECULAR CHAPERONE HDJ-1; MOLECULAR CHAPERONE
1287	1hdj		7	69	1.6e-27	1.26	1.00		HUMAN HSP40; CHAIN: NULL;	MOLECULAR CHAPERONE HDJ-1; MOLECULAR CHAPERONE
1292	1pbw	A	112	300	6.4e-08			93.22	PHOSPHATIDYLINOSITOL 3-KINASE; CHAIN: A, B;	PHOSPHOTRANSFERASE RHOGAP DOMAIN; PHOSPHOTRANSFERASE, TPASE ACTIVATING PROTEIN, GAP, CDC42, 2 PHOSPHOINOSITIDE 3-KINASE, SH3 DOMAIN, SH2 DOMAIN, 3 SIGNAL TRANSDUCTION
1292	1pbw	B	112	314	8e-09			94.15	PHOSPHATIDYLINOSITOL 3-KINASE; CHAIN: A, B;	PHOSPHOTRANSFERASE RHOGAP DOMAIN; PHOSPHOTRANSFERASE, TPASE ACTIVATING PROTEIN, GAP, CDC42, 2 PHOSPHOINOSITIDE 3-KINASE, SH3 DOMAIN, SH2 DOMAIN, 3 SIGNAL TRANSDUCTION
1292	1rgp		99	288	4.8e-17			109.76	RHOGAP; CHAIN: NULL;	G-PROTEIN CDC42 GTPASE-ACTIVATING PROTEIN; G-PROTEIN, GAP, SIGNAL-TRANSDUCTION
1292	1tx4	A	105	302	1.1e-17			114.46	P50-RHOGAP; CHAIN: A; TRANSFORMING PROTEIN	COMPLEX(GTPASE ACTIVATN/PROTO-ONCOGENE)

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									RHOA; CHAIN: B;	GTPASE-ACTIVATING PROTEIN RHO GAP; COMPLEX (GTPASE ACTIVATION/PROTO-ONCOGENE), GTPASE, 2 TRANSITION STATE, GAP
1293	1bqq	M	112	281	9.6e-54			103.34	MEMBRANE-TYPE MATRIX METALLOPROTEINASE; CHAIN: M; METALLOPROTEINASE INHIBITOR; CHAIN: T;	COMPLEX (METALLOPROTEINASE/RECEPTOR) CDMT1-MMP; TIMP-2 MATRIX METALLOPROTEINASE, TISSUE INHIBITOR OF 2 METALLOPROTEINASES, PROTEINASE COMPLEX, PRO-GELATINASE A 3 ACTIVATOR, CRYSTAL STRUCTURE, COMPLEX 4 (METALLOPROTEINASE/RECEPTOR)
1293	1cge		110	254	8e-60			120.96	HYDROLASE (METALLOPROTEASE) COLLAGENASE (E.C.3.4.24.7) (CATALYTIC DOMAIN) CRYSTAL FORM I ICGE 3	
1293	1ciz	A	107	272	4.8e-63			132.96	STROMELYSIN-1; CHAIN: A;	METALLOPROTEINASE MATRIX METALLOPROTEINASE-3; MATRIX METALLOPROTEINASE, MMP-3, NON-PEPTIDE INHIBITOR
1293	1ck7	A	25	699	0			647.13	GELATINASE A; CHAIN: A;	HYDROLASE MMP-2, 72KD TYPE IV COLLAGENASE; HYDROLASE (METALLOPROTEASE), FULL-LENGTH, METALLOPROTEINASE, 2 GELATINASE A
1293	1cxw	A	274	333	9.6e-14			90.80	HUMAN MATRIX METALLOPROTEINASE 2; CHAIN: A;	HYDROLASE COL-2; BETA SHEET, ALPHA HELIX, HYDROLASE
1293	1fbl		107	449	3.2e-70			151.00	FIBROBLAST (INTERSTITIAL)	METALLOPROTEASE

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1293	lgen		474	699	9.6e-50			99.59	COLLAGENASE (MMP-1); IFBL 4 CHAIN: NULL; IFBL 5 GELATINASE A; CHAIN: NULL;	HYDROLASE (METALLOPROTEASE) MMP-2, 72KD TYPE IV COLLAGENASE; HYDROLASE, HEMOPEXIN DOMAIN, HYDROLASE, METALLOPROTEASE
1293	lhfc		115	265	8e-60			117.07	METALLOPROTEASE FIBROBLAST COLLAGENASE (E.C.3.4.24.7) IHFC 3	
1293	lmmq		107	279	8e-56			119.28	MATRILYSIN; IMMQ 5 CHAIN: NULL; IMMQ 6	METALLOPROTEASE MMP-9, PUMP-1, MATRIN; IMMQ 7
1293	lpex		477	699	4.8e-63			84.70	COLLAGENASE-3; CHAIN: NULL;	METALLOPROTEASE MMP-13; C-TERMINAL HEMOPEXIN-LIKE DOMAIN OF MATRIX-METALLOPROTEINASE
1293	lqib	A	112	272	1.6e-57			144.06	GELATINASE A; CHAIN: A;	HYDROLASE MATRIX METALLOPROTEINASE-2; INHIBITOR, MATRIN, MATRIX METALLOPROTEINASE-2 (MMP-2), 2 GELATINASE A, METZINCIN, HYDROLASE
1293	lslm		44	272	1.6e-82			187.06	STROMELYSIN-1; CHAIN: NULL;	HYDROLASE MATRIX METALLOPROTEINASE-3, PROTEOGLYCANASE; HYDROLASE, METALLOPROTEASE, FIBROBLAST, COLLAGEN DEGRADATION
1293	830c	A	107	267	1.6e-59			138.28	MMP-13; CHAIN: A, B;	MATRIX METALLOPROTEASE MMP-13; MATRIX METALLOPROTEASE
1294	1ek7	A	25	432	0			419.38	GELATINASE A; CHAIN: A;	HYDROLASE MMP-2, 72KD TYPE IV COLLAGENASE; HYDROLASE (METALLOPROTEASE), FULL-

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1294	1cxw	A	274	333	3.2e-21			90.47	HUMAN MATRIX METALLOPROTEINASE 2; CHAIN: A;	LENGTH, METALLOPROTEINASE, 2 GELATINASE A
1297	2ucz		400	562	3.2e-44			80.92	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	HYDROLASE COL-2; BETA SHEET, ALPHA HELIX, HYDROLASE
1298	1bih	A	1462	1834	8e-44			176.45	HEMOLIN; CHAIN: A, B;	UBIQUITIN CONJUGATION UBC7; UBIQUITIN CONJUGATION, LIGASE, YEAST
1298	1fnf		1660	2042	8e-18			104.50	FIBRONECTIN; 1FNF 6 CHAIN: NULL; 1FNF 7	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1298	1itb	B	1370	1645	3.2e-18			104.57	INTERLEUKIN-1 BETA; CHAIN: A; TYPE 1 INTERLEUKIN-1 RECEPTOR; CHAIN: B;	CELL ADHESION PROTEIN RGD, EXTRACELLULAR MATRIX 1FNF 18
1301	1agr	E	45	172	4.8e-48			146.45	GUANINE NUCLEOTIDE-BINDING PROTEIN G(I); CHAIN: A, D; RGS4; CHAIN: E, H;	COMPLEX (SIGNAL TRANSDUCTION/REGULATOR) GL-ALPHA-1; REGULATOR OF G-PROTEIN SIGNALING 4; GL-ALPHA-1, HYDROLASE, SIGNAL TRANSDUCTION, RGS4, 2 COMPLEX (SIGNAL TRANSDUCTION/REGULATOR), GTP-BINDING, 3 GTPASE ACTIVATING PROTEIN
1301	1agr	H	54	169	6.4e-43			133.76	GUANINE NUCLEOTIDE-	COMPLEX (SIGNAL

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									BINDING PROTEIN G(I); CHAIN: A, D; RGS4; CHAIN: E, H;	TRANSDUCTION/REGULATOR) GI-ALPHA-1; REGULATOR OF G-PROTEIN SIGNALLING 4; GI-ALPHA-1, HYDROLASE, SIGNAL TRANSDUCTION, RGS4, 2 COMPLEX (SIGNAL TRANSDUCTION/REGULATOR), GTP-BINDING, 3 GTPASE ACTIVATING PROTEIN
1301	1cmz	A	46	172	3.2e-46			121.40	GAIP (G-ALPHA INTERACTING) PROTEIN; CHAIN: A;	SIGNALING PROTEIN REGULATION GALPHA INTERACTING PROTEIN; GAIP, RGS, REGULATOR OF G PROTEIN, SIGNALING PROTEIN 2 REGULATION
1302	1a4i	A	5	235	4.8e-74			94.97	METHYLENETETRAHYDROFO LATE DEHYDROGENASE / CHAIN: A, B;	OXIDOREDUCTASE METHYLENETHF DEHYDROGENASE / METHENYLTHF THF, BIFUNCTIONAL, DEHYDROGENASE, CYCLOHYDROLASE, FOLATE, 2 OXIDOREDUCTASE HEADER
1302	1b0a	A	1	235	8e-77			106.54	FOLD BIFUNCTIONAL PROTEIN; CHAIN: A;	OXIDOREDUCTASE, HYDROLASE FOLATE, DEHYDROGENASE, CYCLOHYDROLASE, BIFUNCTIONAL, 2 CHANNELING, OXIDOREDUCTASE, HYDROLASE
1307	1awc	B	18	157	8e-34	-0.23	0.52		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1307	1awc	B	3	125	4.8e-29	-0.09	0.29		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1307	1bd8		21	160	8e-27	-0.01	0.19		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1307	1bi7	B	443	560	6.4e-17	0.14	0.04		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR; CHAIN: B;	COMPLEX (KINASE/ANTI-ONCOGENE) CDK6; P16INK4A, MTS1; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, MULTIPLE TUMOR SUPPRESSOR, 3 MTS1, COMPLEX (KINASE/ANTI-ONCOGENE) HEADER
1307	1blx	B	21	160	6.4e-26	-0.17	0.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1307	1blx	B	50	183	1.3e-23	0.01	0.37		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1307	1bu9	A	1	130	6.4e-25	-0.12	0.15		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	(INHIBITOR PROTEIN/KINASE) HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1307	1d9s	A	443	567	1.6e-17	0.14	0.06		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
1307	1ihb	A	18	161	1.3e-25	-0.12	0.10		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1307	1ihb	A	1	129	3.2e-24	0.01	0.37		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1307	1myo		19	127	1.6e-20	0.14	0.01		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
1314	1by2		26	138	1.1e-44			112.99	MAC-2 BINDING PROTEIN; CHAIN: NULL;	EXTRACELLULAR MODULE TUMOR-ASSOCIATED ANTIGEN 90K; EXTRACELLULAR MODULE, SCAVENGER RECEPTOR, TUMOUR-ASSOCIATED 2 ANTIGEN, EXTRACELLULAR MATRIX, GLYCOSYLATED PROTEIN
1315	1ael	A	34	304	1.6e-66			73.73	TROPINONE REDUCTASE-I; CHAIN: A, B;	OXIDOREDUCTASE OXIDOREDUCTASE, TROPANE ALKALOID BIOSYNTHESIS, REDUCTION OF 2 TROPINONE TO TROPINE, SHORT-CHAIN

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1315	lael	B	34	304	9.6e-68			76.92	TROPINONE REDUCTASE-I; CHAIN: A, B;	DEHYDROGENASE
1315	lbdb		35	314	1.6e-47			65.57	CIS-BIPHENYL-2,3-DIHYDRODIOL-2,3-DEHYDROGENASE; CHAIN: NULL;	OXIDOREDUCTASE NAD-DEPENDENT OXIDOREDUCTASE, SHORT-CHAIN ALCOHOL 2 DEHYDROGENASE, PCB DEGRADATION
1315	leyd	A	35	297	3.2e-54			69.13	CARBONYL REDUCTASE; CHAIN: A, B, C, D;	OXIDOREDUCTASE SHORT-CHAIN DEHYDROGENASE, OXIDOREDUCTASE
1315	lfds		38	319	4.8e-32			79.80	17-BETA-HYDROXYSTEROID-DEHYDROGENASE; CHAIN: NULL;	DEHYDROGENASE
1315	lfmc	A	30	298	6.4e-66			82.26	7 ALPHA-HYDROXYSTEROID DEHYDROGENASE; CHAIN: A, B;	DEHYDROGENASE, 17-BETA-HYDROXYSTEROID
1315	lhdc	A	35	306	4.8e-67			74.82	OXIDOREDUCTASE 3-ALPHA, 20-BETA-HYDROXYSTEROID DEHYDROGENASE (E.C.1.1.1.53) IHDC 3 COMPLEXED WITH CARBENOXOLONE IHDC 4	OXIDOREDUCTASE SHORT-CHAIN DEHYDROGENASE/REDUCTASE, BILE ACID CATABOLISM
1315	loaa		35	297	3.2e-21			65.22	SEPIAPTERIN REDUCTASE; CHAIN: NULL;	OXIDOREDUCTASE SEPIAPTERIN REDUCTASE, TETRAHYDROBIOPTERIN, OXIDOREDUCTASE
1315	lybv	A	24	308	3.2e-61			82.44	TRIHYDROXYNAPHTHALENE REDUCTASE; CHAIN: A, B;	OXIDOREDUCTASE NAPHTHOL REDUCTASE; OXIDOREDUCTASE
1315	2ae2	A	32	291	9.6e-65			76.67	TROPINONE REDUCTASE-II;	OXIDOREDUCTASE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									CHAIN: A, B;	OXIDOREDUCTASE, TROPANE ALKALOID BIOSYNTHESIS, REDUCTION OF 2 TROPINONE TO PSEUDOTROPINE, SHORT-CHAIN DEHYDROGENASE
1321	1pbk		224	339	1.3e-24			194.11	FKBP25; CHAIN: NULL;	ISOMERASE FKBP25 C-TERMINAL DOMAIN; FKBP12 HOMOLOGOUS DOMAIN OF HFKB25, ISOMERASE
1323	1am4	D	31	218	3.2e-43			50.20	P50-RHO GAP; CHAIN: A, B, C; CDC42HS; CHAIN: D, E, F;	COMPLEX (GTPASE-ACTIVATING/GTP-BINDING) COMPLEX (GTPASE-ACTIVATING/GTP-BINDING), GTPASE ACTIVATION
1323	1byu	A	29	244	3.2e-32			61.74	GTP-BINDING PROTEIN RAN; CHAIN: A, B;	TRANSPORT PROTEIN TC4; GTPASE, NUCLEAR TRANSPORT, TRANSPORT PROTEIN
1323	1byu	B	27	245	4.8e-33			64.26	GTP-BINDING PROTEIN RAN; CHAIN: A, B;	TRANSPORT PROTEIN TC4; GTPASE, NUCLEAR TRANSPORT, TRANSPORT PROTEIN
1323	1cly	A	31	203	4.8e-64			79.57	RAS-RELATED PROTEIN RAP-1A; CHAIN: A; PROTO-ONCOGENE SERINE/THREONINE PROTEIN KINASE CHAIN: B;	SIGNALING PROTEIN GTP-BINDING PROTEINS, PROTEIN-PROTEIN COMPLEX, EFFECTORS
1323	1ctq	A	33	204	1.3e-64			93.92	TRANSFORMING PROTEIN P21/H-RAS-1; CHAIN: A;	SIGNALING PROTEIN G PROTEIN, GTP HYDROLYSIS, KINETIC CRYSTALLOGRAPHY, 2 SIGNALING PROTEIN
1323	1cxz	A	28	204	1.6e-50			52.92	HIS-TAGGED TRANSFORMING PROTEIN RHOA(0-181); CHAIN: A; PKN; CHAIN: B;	SIGNALING PROTEIN-PROTEIN COMPLEX, ANTIPARALLEL COILED-COIL
1323	1ibr	A	34	209	1.1e-31			60.48	RAN; CHAIN: A, C; IMPORTIN	SMALL GTPASE KARYOPHERIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									BETA SUBUNIT; CHAIN: B, D;	BETA, P95 SMALL GTPASE, NUCLEAR TRANSPORT RECEPTOR
1323	lkao		31	204	6.4e-61			91.54	RAP2A; CHAIN: NULL;	GTP-BINDING PROTEIN GTP-BINDING PROTEIN, SMALL G PROTEIN, RAP2, GDP, RAS
1323	lmhl		30	222	1.6e-51			62.77	RAC1; CHAIN: NULL;	GTP-BINDING GTP-BINDING, GTPASE, SMALL G-PROTEIN, RHO FAMILY, RAS SUPER 2 FAMILY
1323	lrrp	C	31	227	1.1e-31			59.75	RAN; CHAIN: A, C; NUCLEAR PORE COMPLEX PROTEIN NUP358; CHAIN: B, D;	COMPLEX (SMALL GTPASE/NUCLEAR PROTEIN) COMPLEX (SMALL GTPASE/NUCLEAR PROTEIN), SMALL GTPASE, 2 NUCLEAR TRANSPORT
1323	lzbld	A	29	209	9.6e-58			63.61	RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;	COMPLEX (GTP-BINDING/EFFECTOR) RAS-RELATED PROTEIN RAB3A; COMPLEX (GTP-BINDING/EFFECTOR), G PROTEIN, EFFECTOR, RABCD, 2 SYNAPTIC EXOCYTOSIS, RAB PROTEIN, RAB3A, RABPHILIN
1323	2nrg	A	33	230	1.6e-46			57.05	GTP BINDING PROTEIN (G25K); CHAIN: A; GTPASE ACTIVATING PROTEIN (RHG); CHAIN: B;	HYDROLASE CDC42/CDC42GAP; CDC42/CDC42GAP; TRANSITION STATE, G-PROTEIN; GAP, CDC42, ALF3, HYDROLASE
1323	3rab	A	30	204	1.6e-58			67.16	RAB3A; CHAIN: A;	HYDROLASE G PROTEIN, VESICULAR TRAFFICKING, GTP HYDROLYSIS, RAB 2 PROTEIN, NEUROTRANSMITTER RELEASE, HYDROLASE
1324	1a6o		167	536	1.6e-80			107.93	PROTEIN KINASE CK2/ALPHA-SUBUNIT; CHAIN: NULL;	TRANSFERASE TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, CASEIN KINASE, 2

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1324	1aq1		196	503	0			129.21	CYCLIN-DEPENDENT PROTEIN KINASE 2; CHAIN: NULL;	SER/THR KINASE PROTEIN KINASE CDK2; PROTEIN KINASE, CELL CYCLE, PHOSPHORYLATION, STAUROSPORINE, 2 CELL DIVISION, MITOSIS, INHIBITION
1324	1bi8	A	197	493	1.6e-81			122.05	CYCLIN-DEPENDENT KINASE 6; CHAIN: A, C; CYCLIN-DEPENDENT KINASE INHIBITOR; CHAIN: B, D;	COMPLEX (KINASE/INHIBITOR) CDK6; P19INK4D; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, COMPLEX (KINASE/INHIBITOR) HEADER HELIX
1324	1blx	A	192	499	3.2e-91			133.50	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1324	1cmk	E	160	503	8e-48			102.25	PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT 1CMK 3 (E.C.2.7.1.37) 1CMK 4	
1324	1ctp	E	165	503	3.2e-47			102.19	TRANSFERASE(PHOSPHOTRANSFERASE) CAMP-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) 1CTP 3 (CATALYTIC SUBUNIT) 1CTP 4 HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	
1324	1hcl		196	503	0			141.09		PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1324	1ian		180	567	1.6e-97			117.40	P38 MAP KINASE; CHAIN: NULL;	SERINE/THREONINE-PROTEIN KINASE CSBP, RK, P38; PROTEIN SER/THR-KINASE, SERINE/THREONINE-PROTEIN KINASE
1324	1jnk		180	563	9.6e-100			136.35	C-JUN N-TERMINAL KINASE; CHAIN: NULL;	TRANSFERASE JNK3; TRANSFERASE, JNK3 MAP KINASE, SERINE/THREONINE PROTEIN 2 KINASE
1324	1kob	A	170	522	1.6e-51			105.97	TWITCHIN; CHAIN: A, B;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
1324	1p38		179	570	0			150.88	MAP KINASE P38; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE; TRANSFERASE, MAP KINASE, SERINE/THREONINE-PROTEIN KINASE, 2 P38
1324	1pme		190	568	0			128.64	ERK2; CHAIN: NULL;	TRANSFERASE MAP KINASE, SERINE/THREONINE PROTEIN KINASE, TRANSFERASE
1324	3erk		181	509	0			140.27	EXTRACELLULAR REGULATED KINASE 2; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE, MAP 2, ERK2; TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, MAP KINASE, 2 ERK2
1325	1a6o		167	496	6.4e-80			108.11	PROTEIN KINASE CK2/ALPHA-SUBUNIT; CHAIN: NULL;	TRANSFERASE TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, CASEIN KINASE, 2 SER/THR KINASE
1325	1aq1		196	503	0			129.37	CYCLIN-DEPENDENT PROTEIN KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; PROTEIN KINASE, CELL CYCLE, PHOSPHORYLATION, STAUROSPORINE, 2 CELL DIVISION, MITOSIS, INHIBITION

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQBOLD score	Compound	PDB annotation
1325	1bi8	A	197	493	8e-86			122.26	CYCLIN-DEPENDENT KINASE 6; CHAIN: A, C; CYCLIN-DEPENDENT KINASE INHIBITOR; CHAIN: B, D;	COMPLEX (KINASE/INHIBITOR) CDK6; P19INK4D; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, COMPLEX (KINASE/INHIBITOR) HEADER HELIX
1325	1blx	A	192	499	1.3e-94			133.76	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1325	1cmk	E	160	503	3.2e-49			102.41	PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT 1CMK 3 (E.C.2.7.1.37) 1CMK 4	
1325	1ctp	E	165	503	3.2e-49			102.34	TRANSFERASE(PHOSPHOTRANSFERASE) CAMP-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) 1CTP 3 (CATALYTIC SUBUNIT) 1CTP 4	
1325	1hcl		196	503	0			141.19	HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION
1325	1ian		180	567	0			118.03	P38 MAP KINASE; CHAIN: NULL;	SERINE/THREONINE-PROTEIN KINASE CSBP, RK, P38; PROTEIN SER/THR-KINASE, SERINE/THREONINE-PROTEIN KINASE
1325	1jnk		180	563	4.8e-100			136.46	C-JUN N-TERMINAL KINASE;	TRANSFERASE JNK3;

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									CHAIN: NULL;	TRANSFERASE, JNK3 MAP KINASE, SERINE/THREONINE PROTEIN 2 KINASE
1325	1kob	A	170	522	9.6e-53			106.60	TWITCHIN; CHAIN: A, B;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
1325	1p38		179	570	0			151.09	MAP KINASE P38; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE; TRANSFERASE, MAP KINASE, SERINE/THREONINE-PROTEIN KINASE, 2 P38
1325	1pme		190	568	0			128.85	ERK2; CHAIN: NULL;	TRANSFERASE MAP KINASE, SERINE/THREONINE PROTEIN KINASE, TRANSFERASE
1325	1tki	A	194	519	1.1e-44			99.53	TITIN; CHAIN: A, B;	SERINE KINASE SERINE KINASE, TITIN, MUSCLE, AUTOINHIBITION
1325	3erk		181	509	0			140.42	EXTRACELLULAR REGULATED KINASE 2; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE, MAP 2, ERK2; TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, MAP KINASE, 2 ERK2
1327	1cs8	A	1	350	0			368.72	HUMAN PROCATHEPSIN L; CHAIN: A;	HYDROLASE PROSEGMENT, PROPEPTIDE, INHIBITION, HYDROLASE
1328	1cs8	A	19	391	0			412.39	HUMAN PROCATHEPSIN L; CHAIN: A;	HYDROLASE PROSEGMENT, PROPEPTIDE, INHIBITION, HYDROLASE
1333	1edh	A	65	269	8e-50			124.30	E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1333	1ncj	A	64	268	8e-52			129.50	N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
1335	1adl		3	133	9.6e-56			158.94	LIPID-BINDING PROTEIN ADIPOCYTE LIPID-BINDING PROTEIN COMPLEXED WITH ARACHIDONIC 1ADL 3 ACID 1ADL 4	
1335	1hmr		3	133	6.4e-58			146.24	LIPID-BINDING PROTEIN FATTY ACID BINDING PROTEIN (HUMAN MUSCLE, M-FABP) COMPLEXED 1HMR 3 WITH ONE MOLECULE OF ELAIDIC ACID 1HMR 4	
1335	1pmp	A	3	133	3.2e-55			161.49	CELLULAR LIPOPHILIC TRANSPORT PROTEIN P2 MYELIN PROTEIN (P2) 1PMP 3	
1340	1a12	A	11	409	1.6e-78			141.30	REGULATOR OF CHROMOSOME CONDENSATION 1; CHAIN: A, B, C;	GUANINE NUCLEOTIDE EXCHANGE FACTOR RCC1; GUANINE NUCLEOTIDE EXCHANGE FACTOR, GEF, RAN, 2 RAS-LIKE NUCLEAR GTP BINDING PROTEIN HEADER TER
1345	1a45		1	148	1.4e-61			122.87	GAMMAF CRYSTALLIN; CHAIN: NULL	EYE LENS PROTEIN EYE LENS PROTEIN
1345	1a5d	A	1	148	4.8e-63			121.88	GAMMAE CRYSTALLIN; CHAIN: A, B	EYE LENS PROTEIN EYE LENS PROTEIN
1345	1am m		1	148	3.2e-65			125.68	GAMMA B-CRYSTALLIN; CHAIN: NULL;	CRYSTALLIN GAMMA II-CRYSTALLIN EYE LENS PROTEIN, CRYSTALLIN
1345	1bd7	A	1	147	1.6e-39			80.96	CIRCULARLY PERMUTED BB2-CRYSTALLIN; CHAIN: A, B;	EYE-LENS PROTEIN EYE-LENS PROTEIN, BETA-CRYSTALLIN B,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										EYE-LENS PROTEIN, 2 MULTIGENE FAMILY
1345	1elp	A	1	148	1.3e-62			122.84	GAMMA-D CRYSTALLIN; CHAIN: A, B	EYE LENS PROTEIN EYE LENS PROTEIN
1345	1got	B	48	388	9.6e-31			60.77	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
1345	2bb2		1	148	1.6e-47			99.58	EYE LENS PROTEIN BETA-B2-CRYSTALLIN 2BB2 3	
1352	2fha		6	177	8e-73			273.99	FERRITIN; CHAIN: NULL;	IRON STORAGE IRON STORAGE
1353	1qub	A	184	484	1.6e-11			84.05	HUMAN BETA2-GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI-DOMAIN, MEMBRANE ADHESION
1363	1awc	B	38	192	1.6e-39			64.05	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1363	1bd8		2	161	8e-30			54.79	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1363	1blx	B	1	165	8e-29			55.34	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1363	1bu9	A	31	212	1.6e-34			54.53	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1363	1ihb	A	5	162	8e-34			54.88	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1363	1ikn	D	73	307	4.8e-38			67.03	NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1363	1myo		39	156	3.2e-25			53.66	MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
1363	1nfi	E	31	243	1.6e-38			64.27	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1366	1dqy	A	143	415	8.5e-91	0.64	1.00		SYNAPTOTAGMIN III; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS BETA SANDWICH, CALCIUM ION, C2 DOMAIN
1366	1dqy	A	144	415	3.2e-46	0.49	1.00		SYNAPTOTAGMIN III; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS BETA SANDWICH, CALCIUM ION, C2 DOMAIN

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1366	lrsy		134	270	3.4e-40	0.40	1.00		CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN 1 (FIRST C2 DOMAIN) (CALB) IRSY 3	
1366	lrsy		134	270	3.4e-40			122.64	CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN 1 (FIRST C2 DOMAIN) (CALB) IRSY 3	
1368	lbu7	A	42	505	1.6e-92			197.06	CYTOCHROME P450; CHAIN: A, B;	OXIDOREDUCTASE FATTY ACID HYDROXYLASE; FATTY ACID MONOOXYGENASE, HEMOPROTEIN, P450 REMARK
1368	loxa		23	504	3.2e-31			67.59	CYTOCHROME P450 ERYF; 10XA 5 CHAIN: NULL 10XA 6	OXIDOREDUCTASE (OXYGENASE)
1372	lbg2		2	340	8e-89			210.20	KINESIN; CHAIN: NULL;	MOTOR PROTEIN MOTOR PROTEIN, ATPASE, MICROTUBULE ASSOCIATED
1372	lbg2		4	340	8e-89	0.54	1.00		KINESIN; CHAIN: NULL;	MOTOR PROTEIN MOTOR PROTEIN, ATPASE, MICROTUBULE ASSOCIATED
1372	lcz7	A	1	340	6.8e-79	0.65	1.00		MICROTUBULE MOTOR PROTEIN NCD; CHAIN: A, B, C, D;	CONTRACTILE PROTEIN NCD, CLARET SEGREGATIONAL PROTEIN; NCD CRYSTAL STRUCTURE, MICROTUBULE MOTORS, KINESIN 2 SUPERFAMILY, CONTRACTILE PROTEIN
1372	lcz7	A	1	341	3.2e-72	0.46	1.00		MICROTUBULE MOTOR PROTEIN NCD; CHAIN: A, B, C, D;	CONTRACTILE PROTEIN NCD, CLARET SEGREGATIONAL PROTEIN; NCD CRYSTAL STRUCTURE, MICROTUBULE MOTORS, KINESIN 2 SUPERFAMILY, CONTRACTILE PROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1372	1cz7	A	1	342	6.8e-79			156.19	MICROTUBULE MOTOR PROTEIN NCD; CHAIN: A, B, C, D;	CONTRACTILE PROTEIN NCD, CLARET SEGREGATIONAL PROTEIN; NCD CRYSTAL STRUCTURE, MICROTUBULE MOTORS, KINESIN 2 SUPERFAMILY, CONTRACTILE PROTEIN
1372	2kin	A	2	252	1.2e-58			139.58	KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1372	2kin	A	4	252	3.2e-57	0.25	1.00		KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1372	2kin	A	6	252	1.2e-58	0.29	1.00		KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1372	2kin	B	265	352	3.4e-28	-0.01	0.98		KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1372	2kin	B	265	358	8e-27	-0.02	0.99		KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1372	2ncd	A	1	339	1.6e-72	0.46	1.00		KINESIN MOTOR NCD; CHAIN: A;	CONTRACTILE PROTEIN KINESIN, MICROTUBULE-BASED MOTOR, NCD, CONTRACTILE PROTEIN
1372	2ncd	A	1	340	1.6e-72			152.53	KINESIN MOTOR NCD; CHAIN: A;	CONTRACTILE PROTEIN KINESIN, MICROTUBULE-BASED MOTOR, NCD, CONTRACTILE PROTEIN
1372	3kar		5	338	5.1e-74			185.05	KINESIN-LIKE PROTEIN KAR3; CHAIN: NULL;	CONTRACTILE PROTEIN KINESIN-RELATED PROTEIN, MOTOR 2 PROTEIN, ATPASE, P-LOOP, MICROTUBULE BINDING PROTEIN
1372	3kar		6	339	6.4e-72	0.31	1.00		KINESIN-LIKE PROTEIN KAR3; CHAIN: NULL;	CONTRACTILE PROTEIN KINESIN-RELATED PROTEIN, MOTOR 2 PROTEIN, ATPASE, P-LOOP, MICROTUBULE BINDING PROTEIN

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1372	3kar		7	338	5.1e-74	0.50	1.00		KINESIN-LIKE PROTEIN KAR3; CHAIN: NULL;	CONTRACTILE PROTEIN CONTRACTILE PROTEIN, KAR3, KINESIN-RELATED PROTEIN, MOTOR 2 PROTEIN, ATPASE, P- LOOP, MICROTUBULE BINDING PROTEIN
1372	3kin	B	269	352	1.4e-26	0.19	0.99		KINESIN HEAVY CHAIN; CHAIN: A, B, C, D;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1372	3kin	B	269	384	3.2e-26	-0.10	0.98		KINESIN HEAVY CHAIN; CHAIN: A, B, C, D;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1373	1a4y	A	123	448	4.8e-12	0.19	0.04		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS
1373	1a4y	A	134	545	4.8e-09	0.26	-0.05		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS
1373	1a4y	A	45	361	9.6e-14	0.10	0.00		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS
1373	1a4y	A	63	230	1e-19	0.29	0.37		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1373	1a9n	A	114	264	5.1e-19	0.66	0.42		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	3 REPEATS COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1373	1a9n	A	65	220	3.4e-22	0.43	0.17		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1373	1a9n	A	90	231	3.4e-19	0.55	0.65		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1373	1a9n	C	114	264	3.4e-18	0.48	0.53		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1373	1a9n	C	65	220	1.4e-22	0.24	0.04		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1373	1a9n	C	90	231	3.4e-19	0.66	0.55		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1373	1bih	A	294	387	6.8e-14	0.33	0.77		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1373	1bih	A	295	427	1.7e-10	0.37	0.25		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1373	1bpv		421	506	3.4e-07	-0.04	0.07		TITIN; CHAIN: NULL;	CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1373	1cs6	A	286	388	8.5e-15	0.01	-0.05		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1373	1cs6	A	295	409	3.4e-12	0.31	0.19		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1373	1cvs	C	306	389	8.5e-14	0.65	1.00		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1373	1cvs	D	296	383	1.2e-14	0.29	0.57		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1373	1d0b	A	152	310	6.4e-26	0.02	0.05		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1373	1d0b	A	176	332	8e-24	0.09	-0.15		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1373	1d0b	A	37	211	1.4e-22	0.13	0.57		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1373	1d0b	A	423	547	1.6e-14	0.05	-0.19		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1373	1d0b	A	79	265	8e-22	0.31	0.30		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1373	1dce	A	32	95	9.6e-09	-0.43	0.23		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1373	1dce	A	37	171	8e-08	-0.03	0.15		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE; RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1373	1ds9	A	56	186	1.6e-10	-0.41	0.28		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT; BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1373	1ev2	E	292	383	5.1e-14	0.13	-0.08		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE 1-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1373	1ev2	G	296	387	6.8e-16	0.22	0.13		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE 1-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1373	1fqv	A	64	231	1.7e-13	0.26	0.54		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1373	1fs2	A	53	231	3.4e-18	0.03	0.31		SKP2; CHAIN: A, C; SKP1;	LIGASE CYCLIN A/CDK2-

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									CHAIN: B, D;	ASSOCIATED P45; CYCLIN A/CDK2-ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
1373	lhmf		303	405	1.7e-08	0.39	0.27		T LYMPHOCYTE ADHESION GLYCOPROTEIN CD2 (HUMAN) 1HNF 3	
1373	lnct		292	383	6.8e-19	0.56	0.31		TITIN; CHAIN: NULL;	MUSCLE PROTEIN CONNECTIN, NEXTM5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN
1373	ltmm		305	383	1.7e-16	0.60	0.76		MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) 1TNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) 1TNM 4 1TNM 58	
1373	lttf		424	502	3.4e-07	-0.29	0.40		GLYCOPROTEIN FIBRONECTIN (TENTH TYPE III MODULE) (NMR, 36 STRUCTURES) 1TTF 3	
1373	lvea	A	297	394	1.7e-11	0.46	0.16		HUMAN VASCULAR CELL ADHESION MOLECULE-1; 1VCA 4 CHAIN: A, B; 1VCA 5	CELL ADHESION PROTEIN VCAM-D1,2; 1VCA 6 IMMUNOGLOBULIN SUPERFAMILY, INTEGRIN-BINDING 1VCA 15
1373	lwio	A	280	411	3.4e-12	0.37	0.00		T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: A, B;	GLYCOPROTEIN CD4; IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, T-CELL, 2 MHC LIPOPROTEIN, POLYMORPHISM
1373	lytg	A	132	362	1.1e-09	0.04	-0.14		GTPASE-ACTIVATING PROTEIN RNA1 SCHPO;	TRANSCRIPTION RNAIP; RANGAP; GTPASE-ACTIVATING PROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									CHAIN: A, B;	FOR SPII, GTPASE-ACTIVATING PROTEIN; GAP, RNAIP, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, 3 HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
1373	2bnh		45	359	1.4e-18	0.04	0.03		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1373	2bnh		47	231	1.7e-23	0.13	0.06		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1373	2dli	A	294	396	3.4e-11	0.20	-0.05		MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	IMMUNE SYSTEM P58 NATURAL KILLER CELL RECEPTOR; KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN
1373	3ncm	A	296	383	3.4e-17	0.92	0.35		NEURAL CELL ADHESION MOLECULE, LARGE ISOFORM; CHAIN: A;	CELL ADHESION PROTEIN NCAM MODULE 2; CELL ADHESION, GLYCOPROTEIN, HEPARIN-BINDING, GPI-ANCHOR, 2 NEURAL ADHESION MOLECULE, IMMUNOGLOBULIN FOLD, HOMOPHILIC 3 BINDING, CELL ADHESION PROTEIN
1374	1cun	A	65	293	0.0017			61.31	ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN

SEQ ID NO:	PDB ID	CHAI NID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1374	1ez7	A	1	131	5.1e-34	-0.46	0.66		MICROTUBULE MOTOR PROTEIN NCD; CHAIN: A, B, C, D;	CONTRACTILE PROTEIN NCD, CLARET SEGREGATIONAL PROTEIN; NCD CRYSTAL STRUCTURE, MICROTUBULE MOTORS, KINESIN 2 SUPERFAMILY, CONTRACTILE PROTEIN
1374	1quu	A	53	295	3.4e-05			66.44	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
1374	1sig		36	318	0.0017			65.31	RNA POLYMERASE PRIMARY SIGMA FACTOR; CHAIN: NULL;	TRANSCRIPTION REGULATION SIGMA70; RNA POLYMERASE SIGMA FACTOR, TRANSCRIPTION REGULATION
1374	2kin	A	1	42	5.1e-15	-0.55	0.12		KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1374	2kin	B	55	141	1.7e-27	-0.41	0.81		KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1374	2kin	B	55	154	1.7e-27			65.43	KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1374	3kar		1	127	1e-30	-0.52	0.60		KINESIN-LIKE PROTEIN KAR3; CHAIN: NULL;	CONTRACTILE PROTEIN CONTRACTILE PROTEIN, KAR3, KINESIN-RELATED PROTEIN, MOTOR 2 PROTEIN, ATPASE, P-LOOP, MICROTUBULE BINDING PROTEIN
1374	3kin	B	59	142	6.8e-25	-0.15	0.86		KINESIN HEAVY CHAIN; CHAIN: A, B, C, D;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1374	3kin	B	59	176	6.8e-25			68.48	KINESIN HEAVY CHAIN; CHAIN: A, B, C, D;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1376	1cej	A	323	405	5.1e-19	-0.02	0.03		MEROZOITE SURFACE PROTEIN 1; CHAIN: A;	SURFACE PROTEIN MEROZOITE SURFACE ANTIGEN 1, MAJOR BLOOD-STAGE EGF-LIKE DOMAIN, EXTRACELLULAR, MODULAR

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										PROTEIN, SURFACE 2 ANTIGEN, MALARIA VACCINE COMPONENT, SURFACE PROTEIN
1376	1cej	A	364	435	6.8e-17	-0.11	0.41		MEROZOITE SURFACE PROTEIN 1; CHAIN: A;	SURFACE PROTEIN MEROZOITE SURFACE ANTIGEN 1, MAJOR BLOOD-STAGE EGF-LIKE DOMAIN, EXTRACELLULAR, MODULAR PROTEIN, SURFACE 2 ANTIGEN, MALARIA VACCINE COMPONENT, SURFACE PROTEIN
1376	1cej	A	403	481	5.1e-09	0.08	-0.14		MEROZOITE SURFACE PROTEIN 1; CHAIN: A;	SURFACE PROTEIN MEROZOITE SURFACE ANTIGEN 1, MAJOR BLOOD-STAGE EGF-LIKE DOMAIN, EXTRACELLULAR, MODULAR PROTEIN, SURFACE 2 ANTIGEN, MALARIA VACCINE COMPONENT, SURFACE PROTEIN
1376	1cej	A	45	128	5.1e-21	0.09	0.53		MEROZOITE SURFACE PROTEIN 1; CHAIN: A;	SURFACE PROTEIN MEROZOITE SURFACE ANTIGEN 1, MAJOR BLOOD-STAGE EGF-LIKE DOMAIN, EXTRACELLULAR, MODULAR PROTEIN, SURFACE 2 ANTIGEN, MALARIA VACCINE COMPONENT, SURFACE PROTEIN
1376	1d4v	A	631	733	1.4e-08	0.30	-0.13		TNF-RELATED APOPTOSIS INDUCING LIGAND; CHAIN: B; DEATH RECEPTOR 5; CHAIN: A;	APOPTOSIS TRAIL; DR5; LIGAND-RECEPTOR COMPLEX, TRIMERIC JELLY-ROLL, TNF-R 2 SUPERFAMILY, APOPTOSIS
1376	1dqb	A	181	252	5.1e-14	0.76	0.78		THROMBOMODULIN; CHAIN: A;	MEMBRANE PROTEIN NMR, THROMBIN, EGF MODULE, ANTICOAGULANT, GLYCOSYLATION
1376	1dqb	A	321	406	5.1e-18	0.30	0.15		THROMBOMODULIN; CHAIN: A;	MEMBRANE PROTEIN NMR, THROMBIN, EGF MODULE,

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										ANTICOAGULANT, GLYCOSYLATION
1376	1dqb	A	400	485	5.1e-10	-0.07	0.00		THROMBOMODULIN; CHAIN: A;	MEMBRANE PROTEIN NMR, THROMBIN, EGF MODULE, ANTICOAGULANT, GLYCOSYLATION
1376	1dqb	A	44	131	5.1e-18	0.25	0.21		THROMBOMODULIN; CHAIN: A;	MEMBRANE PROTEIN NMR, THROMBIN, EGF MODULE, ANTICOAGULANT, GLYCOSYLATION
1376	1edm	B	403	433	3.4e-07	-0.14	0.23		FACTOR IX; CHAIN: B, C;	COAGULATION FACTOR CRYSTAL STRUCTURE, EPIDERMAL GROWTH FACTOR, EGF, 2 CALCIUM-BINDING, EGF-LIKE DOMAIN, STRUCTURE AND FUNCTION, 3 HUMAN FACTOR IX, COAGULATION FACTOR
1376	1f7e	A	403	433	5.1e-07	0.09	0.04		BLOOD COAGULATION FACTOR VII; CHAIN: A;	BLOOD CLOTting FACTOR VII, BLOOD COAGULATION, EGF-LIKE DOMAIN, BLOOD 2 CLOTting
1376	1fjs	L	216	254	1.2e-12	0.66	0.23		COAGULATION FACTOR XA; CHAIN: A; COAGULATION FACTOR XA; CHAIN: L;	BLOOD CLOTting PROTEIN INHIBITOR COMPLEX, COAGULATION COFACTOR, PROTEASE
1376	1fjs	L	284	335	3.4e-20	0.27	0.42		COAGULATION FACTOR XA; CHAIN: A; COAGULATION FACTOR XA; CHAIN: L;	BLOOD CLOTting PROTEIN INHIBITOR COMPLEX, COAGULATION COFACTOR, PROTEASE
1376	1fjs	L	327	374	1.7e-17	-0.13	0.25		COAGULATION FACTOR XA; CHAIN: A; COAGULATION FACTOR XA; CHAIN: L;	BLOOD CLOTting PROTEIN INHIBITOR COMPLEX, COAGULATION COFACTOR, PROTEASE
1376	1fjs	L	407	445	1.4e-15	0.08	0.94		COAGULATION FACTOR XA; CHAIN: A; COAGULATION	BLOOD CLOTting PROTEIN INHIBITOR COMPLEX,

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									FACTOR XA; CHAIN: L;	COAGULATION COFACTOR, PROTEASE
1376	1fjs	L	49	90	1.7e-12	0.83	0.59		COAGULATION FACTOR XA; CHAIN: A; COAGULATION FACTOR XA; CHAIN: L;	BLOOD CLOTTING PROTEIN INHIBITOR COMPLEX, COAGULATION COFACTOR, PROTEASE
1376	lhcg	B	217	254	3.4e-12	0.50	0.46		COAGULATION FACTOR BLOOD COAGULATION FACTOR XA IHCG 3	
1376	lhcg	B	286	334	1.2e-18	0.34	0.33		COAGULATION FACTOR BLOOD COAGULATION FACTOR XA IHCG 3	
1376	lhcg	B	407	445	8.5e-15	0.45	0.89		COAGULATION FACTOR BLOOD COAGULATION FACTOR XA IHCG 3	
1376	lhcg	B	49	90	5.1e-12	0.45	0.95		COAGULATION FACTOR BLOOD COAGULATION FACTOR XA IHCG 3	
1376	lkig	L	327	374	3.4e-18	0.01	0.31		FACTOR XA; CHAIN: H, L; ANTICOAGULANT PEPTIDE; CHAIN: I;	COMPLEX (PROTEASE/INHIBITOR) RTAP; GLYCOPROTEIN, SERINE PROTEASE, PLASMA, BLOOD COAGULATION, 2 COMPLEX (PROTEASE/INHIBITOR)
1376	lkig	L	407	445	6.8e-15	-0.06	0.82		FACTOR XA; CHAIN: H, L; ANTICOAGULANT PEPTIDE; CHAIN: I;	COMPLEX (PROTEASE/INHIBITOR) RTAP; GLYCOPROTEIN, SERINE PROTEASE, PLASMA, BLOOD COAGULATION, 2 COMPLEX (PROTEASE/INHIBITOR)
1376	lkig	L	49	90	5.1e-12	0.66	0.34		FACTOR XA; CHAIN: H, L; ANTICOAGULANT PEPTIDE; CHAIN: I;	COMPLEX (PROTEASE/INHIBITOR) RTAP; GLYCOPROTEIN, SERINE PROTEASE, PLASMA, BLOOD COAGULATION, 2 COMPLEX (PROTEASE/INHIBITOR)
1376	lklo		135	322	6.8e-14	0.47	-0.11		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN

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1376	1klo		286	433	1.7e-20	0.16	-0.18		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1376	1klo		626	787	8.5e-10	0.38	0.00		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1376	1pfx	L	121	254	1.7e-14	0.04	0.01		FACTOR IXA; CHAIN: C, L;; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
1376	1pfx	L	289	427	3.4e-27	0.02	0.23		FACTOR IXA; CHAIN: C, L;; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
1376	1pfx	L	41	152	8.5e-26	0.21	0.89		FACTOR IXA; CHAIN: C, L;; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
1376	1qfk	L	131	226	1.4e-22	0.28	0.37		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
1376	1qfk	L	177	252	8.5e-16	0.18	0.72		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE

SEQ ID NO:	PDB ID	CHAI NID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	PROTEASE
1376	1qfk	L	286	389	3.4e-26	-0.11	0.22		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
1376	1qfk	L	326	419	1.5e-21	-0.01	0.29		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
1376	1qfk	L	367	445	1e-18	0.22	0.99		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
1376	1qfk	L	48	141	1.7e-24	0.12	0.92		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
1376	1qfk	L	89	189	6.8e-23	-0.29	0.52		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE

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1376	1qub	A	41	444	1.7e-46	0.02	-0.18		HUMAN BETA2-GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI-DOMAIN, MEMBRANE ADHESION
1376	1rfn	B	175	228	1e-13	0.24	0.35		COAGULATION FACTOR IX; CHAIN: A; COAGULATION FACTOR IX; CHAIN: B;	COAGULATION FACTOR SERINE PROTEINASE, BLOOD COAGULATION, COAGULATION FACTOR
1376	1rfn	B	285	339	3.4e-19	0.29	-0.01		COAGULATION FACTOR IX; CHAIN: A; COAGULATION FACTOR IX; CHAIN: B;	COAGULATION FACTOR SERINE PROTEINASE, BLOOD COAGULATION, COAGULATION FACTOR
1376	1rfn	B	407	445	3.4e-11	0.13	0.94		COAGULATION FACTOR IX; CHAIN: A; COAGULATION FACTOR IX; CHAIN: B;	COAGULATION FACTOR SERINE PROTEINASE, BLOOD COAGULATION, COAGULATION FACTOR
1376	1rfn	B	49	102	8.5e-12	0.67	-0.15		COAGULATION FACTOR IX; CHAIN: A; COAGULATION FACTOR IX; CHAIN: B;	COAGULATION FACTOR SERINE PROTEINASE, BLOOD COAGULATION, COAGULATION FACTOR
1376	1sfp		805	918	3.4e-21	0.64	0.48		ASFP; CHAIN: NULL;	SPERMADHESIN ACIDIC SEMINAL PROTEIN; SPERMADHESIN, BOVINE SEMINAL PLASMA PROTEIN, ACIDIC 2 SEMINAL FLUID PROTEIN, ASFP, CUB DOMAIN, X-RAY CRYSTAL 3 STRUCTURE, GROWTH FACTOR
1376	1spp	B	809	922	3.4e-22	0.37	0.65		MAJOR SEMINAL PLASMA GLYCOPROTEIN PSP-I; CHAIN: A; MAJOR SEMINAL PLASMA GLYCOPROTEIN PSP-II; CHAIN: B	COMPLEX (SEMINAL PLASMA PROTEIN/SPP) SEMINAL PLASMA PROTEINS, SPERMADHESINS, CUB DOMAIN 2 ARCHITECTURE, COMPLEX (SEMINAL PLASMA PROTEIN/SPP)

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1376	1tpg		68	158	1.5e-21	0.05	0.04		T-PLASMINOGEN ACTIVATOR F1-G; ITPG 7 CHAIN: NULL; ITPG 8	PLASMINOGEN ACTIVATION
1376	1xka	L	131	230	1.7e-15	0.09	0.59		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
1376	1xka	L	182	254	1.7e-15	-0.01	0.43		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
1376	1xka	L	286	380	5.1e-20	0.25	0.69		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
1376	1xka	L	367	444	3.4e-19	0.28	0.40		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
1376	1xka	L	48	145	3.4e-22	0.01	0.55		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
1381	1a06		205	530	5.1e-62	-0.04	0.71		CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE; CHAIN: NULL;	KINASE KINASE, SIGNAL TRANSDUCTION, CALCIUM/CALMODULIN
1381	1a06		236	534	5.1e-62			109.19	CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE;	KINASE KINASE, SIGNAL TRANSDUCTION,

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1381	1a6o		194	550	6.8e-40			84.57	CHAIN: NULL; PROTEIN KINASE CK2/ALPHA-SUBUNIT; CHAIN: NULL;	CALCIUM/CALMODULIN TRANSFERASE TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, CASEIN KINASE, 2 SER/THR KINASE
1381	1bi8	A	204	485	5.1e-41	0.21	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A, C; CYCLIN-DEPENDENT KINASE INHIBITOR; CHAIN: B, D;	COMPLEX (KINASE/INHIBITOR) CDK6; P19INK4D; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, COMPLEX (KINASE/INHIBITOR) HEADER HELIX
1381	1blx	A	198	495	1.2e-46			92.79	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1381	1blx	A	199	485	1.2e-46	0.40	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1381	1csn		203	469	6.8e-48	0.06	0.74		CASEIN KINASE-1; ICSN 4	PHOSPHOTRANSFERASE
1381	1ctp	E	169	524	3.4e-71			154.37	TRANSFERASE(PHOSPHOTRANSFERASE) CAMP-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) ICTP 3 (CATALYTIC SUBUNIT) ICTP 4	
1381	1ctp	E	196	498	3.4e-71	0.41	1.00		TRANSFERASE(PHOSPHOTRANSFERASE) CAMP-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) ICTP 3	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1381	1hel		202	495	1.7e-53	0.39	1.00		(CATALYTIC SUBUNIT) ICTP 4 HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION
1381	1hel		202	499	1.7e-53			115.78	HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION
1381	1ian		183	555	3.4e-40			92.87	P38 MAP KINASE; CHAIN: NULL;	SERINE/THREONINE-PROTEIN KINASE CSBP, RK, P38; PROTEIN SER/THR-KINASE, SERINE/THREONINE-PROTEIN KINASE
1381	1ian		203	475	3.4e-40	0.01	0.88		P38 MAP KINASE; CHAIN: NULL;	SERINE/THREONINE-PROTEIN KINASE CSBP, RK, P38; PROTEIN SER/THR-KINASE, SERINE/THREONINE-PROTEIN KINASE
1381	1jnk		185	577	1.7e-46			112.39	C-JUN N-TERMINAL KINASE; CHAIN: NULL;	TRANSFERASE JNK3; TRANSFERASE, JNK3 MAP KINASE, SERINE/THREONINE PROTEIN 2 KINASE
1381	1jnk		203	512	1.7e-46	0.21	1.00		C-JUN N-TERMINAL KINASE; CHAIN: NULL;	TRANSFERASE JNK3; TRANSFERASE, JNK3 MAP KINASE, SERINE/THREONINE PROTEIN 2 KINASE
1381	1kob	A	170	570	1.7e-68			127.80	TWITCHIN; CHAIN: A, B;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
1381	1kob	A	205	493	1.7e-68	0.52	1.00		TWITCHIN; CHAIN: A, B;	KINASE KINASE, TWITCHIN,

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1381	3erk		198	498	8.5e-53	0.54	1.00		EXTRACELLULAR REGULATED KINASE 2; CHAIN: NULL;	INTRASTERIC REGULATION TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE, MAP 2, ERK2; TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, MAP KINASE, 2 ERK2
1381	3erk		213	562	8.5e-53			98.67	EXTRACELLULAR REGULATED KINASE 2; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE, MAP 2, ERK2; TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, MAP KINASE, 2 ERK2
1384	1ao7	E	52	210	9.6e-54	0.39	1.00		HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA-A2 HEAVY CHAIN; CLASS I MHC, T-CELL RECEPTOR, VIRAL PEPTIDE, 2 COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)
1384	1ao7	E	52	210	9.6e-54			128.38	HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA-A2 HEAVY CHAIN; CLASS I MHC, T-CELL RECEPTOR, VIRAL PEPTIDE, 2 COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)
1384	1bd2	E	52	210	3.2e-66	0.48	1.00		HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA A2 HEAVY CHAIN; COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)
1384	1bd2	E	52	210	3.2e-66			143.49	HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA;	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA A2 HEAVY CHAIN; COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	
1384	1bec		52	210	6.4e-66			130.56	14.3.D T CELL ANTIGEN RECEPTOR; 1BEC 5 CHAIN: NULL; 1BEC 6	RECEPTOR T CELL RECEPTOR 1BEC 14
1384	1bec		53	210	6.4e-66	0.49	1.00		14.3.D T CELL ANTIGEN RECEPTOR; 1BEC 5 CHAIN: NULL; 1BEC 6	RECEPTOR T CELL RECEPTOR 1BEC 14
1384	1fyt	E	53	210	8e-60	0.25	1.00		HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR CHAIN: A; HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-1 CHAIN: B; HEMAGGLUTININ HA1 PEPTIDE CHAIN; CHAIN: C; T-CELL RECEPTOR ALPHA CHAIN; CHAIN: D; T-CELL RECEPTOR BETA CHAIN; CHAIN: E;	IMMUNE SYSTEM HLA-DRI, DRA; HLA-DRI, DRB1 0101; TCR HA1.7 ALPHA CHAIN; TCR HA1.7 BETA CHAIN; PROTEIN-PROTEIN COMPLEX, IMMUNOGLOBULIN FOLD
1384	1ter	B	50	210	9.6e-64	0.43	1.00		ALPHA, BETA T-CELL RECEPTOR CHAIN: A, B;	RECEPTOR TCR; T-CELL, RECEPTOR, TRANSMEMBRANE, GLYCOPROTEIN, SIGNAL
1384	1ter	B	51	210	9.6e-64			131.76	ALPHA, BETA T-CELL RECEPTOR CHAIN: A, B;	RECEPTOR TCR; T-CELL, RECEPTOR, TRANSMEMBRANE, GLYCOPROTEIN, SIGNAL
1388	1a4y	A	21	309	3.2e-17	0.04	-0.11		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS
1388	1a9n	A	26	156	3.4e-21	0.43	-0.01		U2 RNA HAIRPIN IV; CHAIN: Q;	COMPLEX (NUCLEAR

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	PROTEIN/RNA COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1388	1a9n	A	46	155	4.8e-06	0.28	0.19		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1388	1a9n	A	4	121	1.5e-20	0.48	0.65		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1388	1a9n	C	24	106	1.3e-05	0.51	0.51		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1388	1a9n	C	26	156	1.2e-21	0.41	-0.08		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1388	1a9n	C	46	155	4.8e-06	0.42	0.06		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1388	1a9n	C	4	121	6.8e-20	0.67	0.89		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1388	1cs6	A	77	280	0.00034	-0.15	0.07		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1388	1d0b	A	19	194	6.4e-27	0.50	0.77		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1388	1d0b	A	4	128	1.4e-12	0.27	0.89		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1388	1d0b	A	63	216	1.4e-25	0.28	0.43		INTERNALIN B; CHAIN: A;	ADHESION CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1388	1d0b	A	87	236	3.2e-25	-0.05	0.04		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1388	1dce	A	21	127	3.2e-11	0.27	0.90		RAB GERANYLGERANYLTRANSFERASE RASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE RASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1388	1dce	A	46	170	1.6e-12	0.59	0.96		RAB GERANYLGERANYLTRANSFERASE RASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE RASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1388	1ds9	A	103	236	6.4e-13	0.08	-0.02		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1388	1fo1	A	41	103	3.2e-06	-0.05	0.40		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1388	1fo1	A	89	171	4.8e-07	-0.06	0.10		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1388	1fo1	B	41	103	3.2e-06	0.26	0.04		NUCLEAR RNA EXPORT	RNA BINDING PROTEIN TAP (NFX1);

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									FACTOR 1; CHAIN: A, B;	RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1388	1fqv	A	1	173	1.4e-09	0.29	-0.08		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1388	1fqv	A	20	213	1.6e-14	0.12	0.10		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1388	1fqv	A	22	298	4.8e-11	0.08	-0.15		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1388	1fs2	A	11	128	3.4e-12	0.21	0.09		SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	LIGASE CYCLIN A/CDK2-ASSOCIATED P45; CYCLIN A/CDK2-ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
1388	1fs2	A	20	213	1.6e-14	0.04	0.03		SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	LIGASE CYCLIN A/CDK2-ASSOCIATED P45; CYCLIN A/CDK2-ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
1388	2bnh		5	131	1.7e-19	0.07	-0.12		RIBONUCLEASE INHIBITOR;	ACETYLATION RNASE INHIBITOR,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: NULL;	RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLTATION, LEUCINE-RICH REPEATS
1388	2bnh		74	439	3.2e-20	0.06	-0.15		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLTATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLTATION, LEUCINE-RICH REPEATS
1389	1klo		476	643	1.6e-13	0.05	-0.20		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1392	1aj4		10	114	3.2e-23	-0.36	0.01		TROPONIN C; CHAIN: NULL;	MUSCLE PROTEIN CTNC; CARDIAC, MUSCLE PROTEIN, REGULATORY, CALCIUM BINDING
1392	1ak8		2	61	3.2e-22	0.21	0.48		CALMODULIN; CHAIN: NULL;	CALCIUM-BINDING PROTEIN CALMODULIN CERIUM TRIC-DOMAIN, RESIDUES 1 - 75; CERIUM-LOADED, CALCIUM-BINDING PROTEIN
1392	1cdm	A	2	117	4.8e-33	-0.32	0.16		CALCIUM-BINDING PROTEIN CALMODULIN COMPLEXED WITH CALMODULIN-BINDING DOMAIN OF 1CDM 3 CALMODULIN-DEPENDENT PROTEIN KINASE II 1CDM 4	
1392	1cll		1	132	3.2e-38			53.74	CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) 1CLL 3	
1392	1cll		2	117	3.2e-38	-0.37	0.11		CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) 1CLL 3	
1392	1dtl	A	10	117	1.6e-21	-0.54	0.12		CARDIAC TROPONIN C; CHAIN: A;	STRUCTURAL PROTEIN HELIX-TURN-HELIX
1392	1exr	A	2	117	1.6e-35	-0.22	0.23		CALMODULIN; CHAIN: A;	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	PsiBlast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1392	1tcf		1	139	3.2e-28			56.30	TROPONIN C; CHAIN: NULL;	CALCIUM-REGULATED MUSCLE CONTRACTION, MUSCLE CONTRACTION, CALCIUM-BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION REGULATORY DOMAIN, CALCIUM-REGULATED 3 MUSCLE CONTRACTION
1392	1tof		2	111	3.2e-28	-0.35	0.11		TROPONIN C; CHAIN: NULL;	CALCIUM-REGULATED MUSCLE CONTRACTION, MUSCLE CONTRACTION, CALCIUM-BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION REGULATORY DOMAIN, CALCIUM-REGULATED 3 MUSCLE CONTRACTION
1392	1tnx		2	111	8e-24	-0.32	0.33		TROPONIN C; ITNX 4 CHAIN: NULL; ITNX 5	CALCIUM-BINDING PROTEIN EF-HAND ITNX 14
1392	1top		1	141	4.8e-28			51.47	CONTRACTILE SYSTEM PROTEIN TROPONIN C ITOP 3	
1392	1top		2	111	4.8e-28	-0.03	0.36		CONTRACTILE SYSTEM PROTEIN TROPONIN C ITOP 3	
1392	1vrk	A	1	135	1.4e-37			51.68	CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
1392	1vrk	A	2	117	1.4e-37	-0.42	0.27		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
1396	1b0x	A	934	1000	1.7e-24	1.07	1.00		EPHA4 RECEPTOR TYROSINE KINASE; CHAIN: A;	TRANSFERASE RECEPTOR TYROSINE KINASE, PROTEIN INTERACTION MODULE, 2

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										DIMERIZATION DOMAIN, TRANSFERASE
1396	1b4f	A	934	999	8.5e-27	0.92	1.00		EPHB2; CHAIN: A, B, C, D, E, F, G, H;	SIGNAL TRANSDUCTION SAM DOMAIN, EPH RECEPTOR, SIGNAL TRANSDUCTION, OLIGOMER
1396	1bj8		431	537	7.5e-22	0.26	0.46		GP130; CHAIN: NULL;	RECEPTOR RECEPTOR, SIGNAL TRANSDUCER OF IL-6 TYPE CYTOKINES, THIRD 2 N-TERMINAL DOMAIN, TRANSMEMBRANE, GLYCOPROTEIN
1396	1bp3	B	328	531	1.5e-25	-0.06	0.01		GROWTH HORMONE; CHAIN: A; PROLACTIN RECEPTOR; CHAIN: B;	HORMONE/GROWTH FACTOR HORMONE, RECEPTOR, HORMONE/GROWTH FACTOR
1396	1bpv		438	536	4.5e-18	0.20	0.60		TTIN; CHAIN: NULL;	CONNECTIN A71, CONNECTIN; TTIN, CONNECTIN, FIBRONECTIN TYPE III
1396	1byg	A	627	899	3e-93			169.44	C-TERMINAL SRC KINASE; CHAIN: A;	TRANSFERASE CSK; PROTEIN KINASE, C-TERMINAL SRC KINASE, PHOSPHORYLATION, 2 STAUROSPORINE, TRANSFERASE
1396	1byg	A	628	897	1.4e-90	0.83	1.00		C-TERMINAL SRC KINASE; CHAIN: A;	TRANSFERASE CSK; PROTEIN KINASE, C-TERMINAL SRC KINASE, PHOSPHORYLATION, 2 STAUROSPORINE, TRANSFERASE
1396	1byg	A	629	898	3e-93	0.64	1.00		C-TERMINAL SRC KINASE; CHAIN: A;	TRANSFERASE CSK; PROTEIN KINASE, C-TERMINAL SRC KINASE, PHOSPHORYLATION, 2 STAUROSPORINE, TRANSFERASE
1396	1c8p	A	437	531	6e-19	0.46	1.00		CYTOKINE RECEPTOR COMMON BETA CHAIN; CHAIN: A;	MEMBRANE PROTEIN BETA SANDWICH, CYTOKINE RECEPTOR, FN3 DOMAIN
1396	1cd9	B	328	524	4.5e-35	0.40	0.07		GRANULOCYTE COLONY-STIMULATING FACTOR; CHAIN: A, C; G-CSF RECEPTOR;	CYTOKINE G-CSF; G-CSF-R; CLASS1 CYTOKINE, HEMATOPOIETIC RECEPTOR, SIGNAL

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1396	1cto		454	531	6e-19	0.32	0.63		CHAIN: B, D; GRANULOCYTE COLONY-STIMULATING FACTOR RECEPTOR; CHAIN: NULL; ERYTHROPOIETIN RECEPTOR; CHAIN: A, B;	TRANSDUCTION BINDING PROTEIN BINDING PROTEIN, CYTOKINE RECEPTOR
1396	1em	A	338	531	4.5e-22	-0.12	0.28			CYTOKINE EBP; ERYTHROPOIETIN RECEPTOR, SIGNAL TRANSDUCTION, CYTOKINE 2 RECEPTOR CLASS 1
1396	1f6f	C	408	531	4.5e-13	-0.05	0.15		PLACENTAL LACTOGEN; CHAIN: A; PROLACTIN RECEPTOR; CHAIN: B, C;	HORMONE/GROWTH FACTOR/HORMONE RECEPTOR 4-HELICAL BUNDLE, ALPHA HELICAL BUNDLE, TERNARY COMPLEX, FN 2 III DOMAINS, BETA SHEET DOMAINS, CYTOKINE-RECEPTOR COMPLEX
1396	1fgk	A	617	900	0			179.56	FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE
1396	1fgk	A	621	895	0	0.91	1.00		FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE
1396	1fgk	B	614	899	0			182.22	FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1396	1fgk	B	620	895	0	0.87	1.00		FGF RECEPTOR 1; CHAIN: A, B;	RECEPTOR, PHOSPHOTRANSFERASE
1396	1fmk		615	903	0	0.88	1.00		TYROSINE-PROTEIN KINASE SRC; CHAIN: NULL;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE
1396	1fna		454	524	1.2e-13	0.39	0.63		CELL ADHESION PROTEIN FIBRONECTIN CELL-ADHESION MODULE TYPE III-10 1FNA 3	PHOSPHOTRANSFERASE C-SRC, P60-SRC; SRC, TYROSINE KINASE, PHOSPHORYLATION, SH2, SH3, 2 PHOSPHOTYROSINE, PROTO-ONCOGENE, PHOSPHOTRANSFERASE
1396	1fnf		322	531	3e-26	0.08	-0.05		FIBRONECTIN; 1FNF 6 CHAIN: NULL; 1FNF 7	CELL ADHESION PROTEIN RGD, EXTRACELLULAR MATRIX 1FNF 18
1396	1fpu	A	623	897	0	0.71	1.00		PROTO-ONCOGENE TYROSINE-PROTEIN KINASE ABL; CHAIN: A, B;	TRANSFERASE P150, C-ABL; KINASE, KINASE INHIBITOR, STI-571, ACTIVATION LOOP
1396	1ir3	A	623	910	0			188.00	INSULIN RECEPTOR; CHAIN: A; PEPTIDE SUBSTRATE; CHAIN: B;	COMPLEX (TRANSFERASE/SUBSTRATE) TYROSINE KINASE, SIGNAL TRANSDUCTION, PHOSPHOTRANSFERASE, 2 COMPLEX (KINASE/PEPTIDE SUBSTRATE/ATP ANALOG), ENZYME, 3 COMPLEX (TRANSFERASE/SUBSTRATE)
1396	1ir3	A	626	910	0	0.81	1.00		INSULIN RECEPTOR; CHAIN: A;	COMPLEX

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									PEPTIDE SUBSTRATE; CHAIN: B;	(TRANSFERASE/SUBSTRATE) TYROSINE KINASE, SIGNAL TRANSDUCTION, PHOSPHOTRANSFERASE, 2 COMPLEX (KINASE/PEPTIDE SUBSTRATE/ATP ANALOG), ENZYME, 3 COMPLEX (TRANSFERASE/SUBSTRATE)
1396	1mfn		331	533	1.3e-25	0.08	0.53		FIBRONECTIN; CHAIN: NULL;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN
1396	1muk	A	31	202	1.5e-83	0.58	1.00		TYROSINE-PROTEIN KINASE RECEPTOR EPH; CHAIN: A;	TRANSFERASE NUK; TRANSFERASE, EPH RECEPTOR TYROSINE KINASE,
1396	1muk	A	31	202	1.5e-83			182.17	TYROSINE-PROTEIN KINASE RECEPTOR EPH; CHAIN: A;	TRANSFERASE NUK; TRANSFERASE, EPH RECEPTOR TYROSINE KINASE,
1396	1qcf	A	610	902	0	0.90	1.00		HAEMATOPHOETIC CELL KINASE (HCK); CHAIN: A;	TYROSINE KINASE TYROSINE KINASE-INHIBITOR COMPLEX, DOWN-REGULATED KINASE, 2 ORDERED ACTIVATION LOOP
1396	1qg3	A	329	534	1.5e-36	0.19	0.22		INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;	STRUCTURAL PROTEIN INTEGRIN, HEMIDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2 PROTEIN
1396	1qg3	A	331	522	6.8e-11	0.03	0.18		INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;	STRUCTURAL PROTEIN INTEGRIN, HEMIDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2 PROTEIN
1396	1qpc	A	621	900	0	0.97	1.00		LCK KINASE; CHAIN: A;	TRANSFERASE ALPHA BETA FOLD
1396	1qr4	A	331	529	1.5e-30	0.27	-0.03		TENASCIN; CHAIN: A, B;	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-III, HEPARIN,

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN
1396	1sgg		934	995	1.7e-25	1.03	1.00		EPHRIIN TYPE-B RECEPTOR 2; CHAIN: NULL;	TYROSINE-PROTEIN KINASE NMR, RECEPTOR OLIGOMERIZATION, EPH RECEPTORS, TYROSINE 2 PHOSPHORYLATION, SIGNAL TRANSDUCTION, TYROSINE-PROTEIN 3 KINASE
1396	1hff		440	524	1e-17	0.13	0.25		GLYCOPROTEIN FIBRONECTIN (TENTH TYPE III MODULE) (NMR, 36 STRUCTURES) ITTF 3	
1396	1vr2	A	622	897	5.1e-98	0.88	1.00		VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR CHAIN: A;	TRANSFERASE KDR; TYROSINE KINASE
1396	2fnb	A	326	423	3e-09	0.07	-0.14		FIBRONECTIN; CHAIN: A;	PROTEIN BINDING ED-B, FIBRONECTIN, TYPEIII DOMAIN, ANGIOGENESIS, PROTEIN 2 BINDING
1396	2fnb	A	439	529	9e-19	0.36	0.17		FIBRONECTIN; CHAIN: A;	PROTEIN BINDING ED-B, FIBRONECTIN, TYPEIII DOMAIN, ANGIOGENESIS, PROTEIN 2 BINDING
1396	2hft		324	524	6e-34	0.22	-0.18		HUMAN TISSUE FACTOR; 2HFT 4 CHAIN: NULL; 2HFT 5	COAGULATION FACTOR
1401	1akh	A	81	121	6e-05	1.11	0.99		MATING-TYPE PROTEIN A-1; CHAIN: A; MATING-TYPE PROTEIN ALPHA-2; CHAIN: B; DNA; CHAIN: C;	COMPLEX (TWO DNA-BINDING PROTEINS/DNA) MAT ALPHA-2; COMPLEX (TWO DNA-BINDING PROTEINS/DNA), COMPLEX, 2 DNA-BINDING PROTEIN, DNA, TRANSCRIPTION REGULATION
1401	1au7	A	83	125	0.00015	0.82	0.94		PIT-1; CHAIN: A, B; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) GHF-1; COMPLEX

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										(DNA-BINDING PROTEIN/DNA), PITUITARY, CPHD, 2 POU DOMAIN, TRANSCRIPTION FACTOR
1401	1b72	B	83	125	0.0006	0.27	0.43		HOMEODOMAIN PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA CHAIN: D; DNA CHAIN: E;	PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA
1401	1bw5		83	125	6e-05	0.73	0.93		INSULIN GENE ENHANCER PROTEIN ISL-1; CHAIN: NULL;	DNA-BINDING PROTEIN ISL-1HD DNA-BINDING PROTEIN, HOMEODOMAIN, LIM DOMAIN
1401	1du6	A	83	127	0.0003	-0.11	0.03		HOMEODOMAIN PROTEIN PBX1; CHAIN: A;	GENE REGULATION PBX1; HOMEODOMAIN
1401	1fjl	B	83	125	0.0003	0.82	0.99		PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION
1401	1hdp		83	125	0.00015	0.50	0.80		DNA-BINDING PROTEIN OCT-2 POU HOMEODOMAIN (NMR, AVERAGE STRUCTURE) 1HDP	
1401	1mn	C	82	125	0.00015	0.63	1.00		MCM1 TRANSCRIPTIONAL REGULATOR; CHAIN: A, B; MAT ALPHA-2 TRANSCRIPTIONAL REPRESSOR; CHAIN: C, D; STE6 OPERATOR DNA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION/HOMEODOMAIN) PHEROMONE RECEPTOR TRANSCRIPTION FACTOR; MATING-TYPE PROTEIN ALPHA-2; TRANSCRIPTIONAL REGULATION, 2 TRANSCRIPTIONAL REPRESSION, 2 DNA-BINDING PROTEIN, COMPLEX (TRANSCRIPTION/HOMEODOMAIN/DNA)
1401	1ocp		83	125	9e-06	0.28	0.84		OCT-3; 1OCP 5 CHAIN: NULL; 1OCP 6	DNA-BINDING PROTEIN
1401	1pog		83	125	0.0001	0.41	0.96		DNA BINDING PROTEIN OCT-1 POU HOMEODOMAIN DNA-BINDING PROTEIN MUTANT	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									WITH IPOG 3 ARG GLY SER HIS MET INSERTED AT THE N-TERMINUS AND ASP ILE IPOG 4 INSERTED AT THE C-TERMINUS (INS(RGSHM-RG),INS(I66-DI) IPOG 5 (NMR, 13 STRUCTURES) IPOG 6	
1403	1a36	A	644	772	5.1e-08	0.03	-0.09		TOPOISOMERASE I; CHAIN: A; DNA; CHAIN: B, C;	COMPLEX (ISOMERASE/DNA) COMPLEX (ISOMERASE/DNA), DNA, TOPOISOMERASE I
1403	1dn1	B	389	556	0.00017	-0.16	0.00		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
1403	1or3	A	527	634	0.00017	-0.13	0.19		APOLIPOPROTEIN E; CHAIN: A;	LIPID BINDING PROTEIN APOE3; LIPID TRANSPORT, HEPARIN-BINDING, PLASMA PROTEIN, HDL, VLDL
1403	1quu	A	367	551	6e-15	-0.12	0.04		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
1404	1c28	A	826	947	1e-27	1.14	0.39		30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN CHAIN: A, B, C;	SERUM PROTEIN ACRP30 C1Q TNF TRIMER ALL-BETA, SERUM PROTEIN
1404	1c28	B	827	947	6e-22	0.71	-0.13		30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN CHAIN: A, B, C;	SERUM PROTEIN ACRP30 C1Q TNF TRIMER ALL-BETA, SERUM PROTEIN
1404	1c28	C	826	947	4.5e-18	0.84	0.43		30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN CHAIN: A, B, C;	SERUM PROTEIN ACRP30 C1Q TNF TRIMER ALL-BETA, SERUM PROTEIN
1404	1cun	A	375	591	6e-12	-0.03	0.29		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL, LINKER REGION, 2 2

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1404	1cun	A	436	651	4.5e-07	0.02	0.03		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1404	1fio	A	292	467	6e-07	-0.08	0.19		SSO1 PROTEIN; CHAIN: A;	MEMBRANE PROTEIN FOUR HELIX BUNDLE, ALPHA HELIX
1404	1hae		120	150	0.0045	0.07	0.11		HEREGULIN-ALPHA; CHAIN: NULL;	GROWTH FACTOR NEU DIFFERENTIATION FACTOR (RAT), ACETYLCHOLINE GROWTH FACTOR
1404	1hre		120	150	0.0045	0.13	0.25		GROWTH FACTOR HEREGULIN-ALPHA (EPIDERMAL GROWTH FACTOR-LIKE DOMAIN) IHRE 3 (NMR, MINIMIZED AVERAGE STRUCTURE) IHRE 4	
1407	1b6c	B	25	129	1.4e-09	-0.26	0.12		FK506-BINDING PROTEIN; CHAIN: A, C, E, G; TGF-B SUPERFAMILY RECEPTOR TYPE I; CHAIN: B, D, F, H;	COMPLEX (ISOMERASE/PROTEIN KINASE) FKBP12; SERINE/THREONINE-PROTEIN KINASE RECEPTOR R4; COMPLEX (ISOMERASE/PROTEIN KINASE), RECEPTOR 2 SERINE/THREONINE KINASE
1407	1fgk	A	22	126	1.7e-05	-0.02	0.04		FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1407	1fmk		22	127	3e-05	0.17	0.36		TYROSINE-PROTEIN KINASE SRC; CHAIN: NULL;	PHOSPHOTRANSFERASE C-SRC, P60-SRC; SRC, TYROSINE KINASE, PHOSPHORYLATION, SH2, SH3, 2 PHOSPHOTYROSINE, PROTO-ONCOGENE, PHOSPHOTRANSFERASE
1407	1fpu	A	22	130	1.5e-05	-0.09	0.18		PROTO-ONCOGENE TYROSINE-PROTEIN KINASE ABL; CHAIN: A, B;	TRANSFERASE P150, C-ABL; KINASE, KINASE INHIBITOR, STI-571, ACTIVATION LOOP
1407	1pme		21	131	7.5e-06	-0.12	0.37		ERK2; CHAIN: NULL;	TRANSFERASE MAP KINASE, SERINE/THREONINE PROTEIN KINASE, TRANSFERASE
1407	1qcf	A	22	129	9e-05	-0.56	0.11		HAEMATOPOETIC CELL KINASE (HCK); CHAIN: A;	TYROSINE KINASE TYROSINE KINASE-INHIBITOR COMPLEX, DOWN-REGULATED KINASE, 2 ORDERED ACTIVATION LOOP
1407	1qpc	A	22	61	7.5e-05	-0.75	0.23		LCK KINASE; CHAIN: A;	TRANSFERASE ALPHA BETA FOLD
1407	3erk		21	126	1.5e-05	-0.35	0.09		EXTRACELLULAR REGULATED KINASE 2; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE, MAP 2, ERK2; TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, MAP KINASE, 2 ERK2
1408	1a44		2	168	4.5e-70	0.60	1.00		PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN; CHAIN: NULL;	LIPID-BINDING PROTEIN PEBP, PBP LIPID-BINDING
1408	1a44		2	168	4.5e-70			267.15	PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN; CHAIN: NULL;	LIPID-BINDING PROTEIN PEBP, PBP LIPID-BINDING
1408	1beh	A	3	168	3e-68	0.89	1.00		PHOSPHATIDYLETHANOLAMINE BINDING PROTEIN; CHAIN: A, B;	LIPID-BINDING LIPID-BINDING, SIGNALLING
1408	1beh	A	3	168	3e-68			271.38	PHOSPHATIDYLETHANOLAMINE BINDING PROTEIN; CHAIN: NULL;	LIPID-BINDING LIPID-BINDING, SIGNALLING

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									A, B;	
1410	1a88	A	47	319	0.00015	0.25	0.90		CHLOROPEROXIDASE L; CHAIN: A, B, C;	HALOPEROXIDASE BROMOPEROXIDASE L, HALOPEROXIDASE L; HALOPEROXIDASE, OXIDOREDUCTASE
1410	1a8s		47	319	9e-08	0.13	0.45		CHLOROPEROXIDASE F; CHAIN: NULL;	HALOPEROXIDASE HALOPEROXIDASE F; HALOPEROXIDASE, OXIDOREDUCTASE, PROPIONATE COMPLEX
1410	1azw	A	11	319	4.5e-05			60.20	PROLINE IMINOPEPTIDASE; CHAIN: A, B;	AMINOPEPTIDASE AMINOPEPTIDASE, PROLINE IMINOPEPTIDASE, SERINE PROTEASE, 2 XANTHOMONAS CAMPESTRIS
1410	1azw	A	47	319	4.5e-05	0.00	0.42		PROLINE IMINOPEPTIDASE; CHAIN: A, B;	AMINOPEPTIDASE AMINOPEPTIDASE, PROLINE IMINOPEPTIDASE, SERINE PROTEASE, 2 XANTHOMONAS CAMPESTRIS
1410	1b6g		12	325	1.5e-08			61.14	HALOALKANE DEHALOGENASE; CHAIN: NULL;	HYDROLASE HYDROLASE, HALOALKANE DEHALOGENASE, ALPHA/BETA-HYDROLASE
1410	1b6g		35	318	1.5e-08	0.13	0.77		HALOALKANE DEHALOGENASE; CHAIN: NULL;	HYDROLASE HYDROLASE, HALOALKANE DEHALOGENASE, ALPHA/BETA-HYDROLASE
1410	1cqW	A	10	319	6e-09	0.38	0.99		HALOALKANE DEHALOGENASE; 1- CHLOROHEXANE CHAIN: A;	HYDROLASE A/B HYDROLASE FOLD, DEHALOGENASE I-S BOND
1410	1cv2	A	47	154	3e-05	-0.16	0.19		HALOALKANE DEHALOGENASE; CHAIN: A;	HYDROLASE LINB, 1,3,4,6- TETRACHLORO-1,4- CYCLOHEXADIENE

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	PsiBlast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										DEHALOGENASE, LINDANE, BIODEGRADATION, ALPHA/BETA-HYDROLASE
1410	1ek1	A	47	321	1.1e-07	0.12	0.98		EPOXIDE HYDROLASE; CHAIN: A, B;	HYDROLASE HOMODIMER, ALPHA/BETA HYDROLASE FOLD, DISUBSTITUTED UREA 2 INHIBITOR
1410	1ek1	B	47	321	3e-07	0.14	0.95		EPOXIDE HYDROLASE; CHAIN: A, B;	HYDROLASE HOMODIMER, ALPHA/BETA HYDROLASE FOLD, DISUBSTITUTED UREA 2 INHIBITOR
1410	1hlg	A	47	165	0.003	-0.15	0.41		LIPASE, GASTRIC; CHAIN: A, B;	HYDROLASE LIPASE
1410	1qge	D	47	195	0.0006	-0.13	0.10		TRIACYLGLYCEROL HYDROLASE; CHAIN: D; TRIACYLGLYCEROL HYDROLASE; CHAIN: E;	HYDROLASE PSEUDOMONADACEAE, CIS-PEPTIDE, CLOSED CONFORMATION, 2 HYDROLASE, LID
1410	1qj4	A	47	316	9e-09	0.02	0.37		HYDROXYNITRILE LYASE; CHAIN: A;	LYASE OXYNITRILE LYASE; OXYNITRILASE, CYANOGENESIS, CYANHYDRIN FORMATION, LYASE
1410	1qtr	A	11	321	1.2e-05			57.92	PROLYL AMINOPEPTIDASE; CHAIN: A;	HYDROLASE ALPHA BETA HYDROLASE FOLD, PROLINE, PROLYL AMINOPEPTIDASE, 2 SERRATIA, IMINOPEPTIDASE
1410	1qtr	A	74	319	1.2e-05	-0.51	0.12		PROLYL AMINOPEPTIDASE; CHAIN: A;	HYDROLASE ALPHA BETA HYDROLASE FOLD, PROLINE, PROLYL AMINOPEPTIDASE, 2 SERRATIA, IMINOPEPTIDASE
1410	4lip	D	47	155	9e-05	0.06	0.05		TRIACYL-GLYCEROL-HYDROLASE; CHAIN: D, E;	LIPASE LIPASE; LIPASE, HYDROLASE, PSEUDOMONADACEAE, COVALENT INTERMEDIATE, 2 TRIGLYCERIDE ANALOGUE, ENANTIOSELECTIVITY
1415	1dn1	B	384	513	0.00045	-0.02	0.09		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									CHAIN: B;	COMPLEX, MULTI-SUBUNIT
1418	1alh	A	401	426	0.00015	0.11	0.01		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1418	1alh	A	404	485	3e-24	0.05	0.95		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1418	lmev	C	403	486	4.5e-25			76.20	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1418	lmev	C	404	485	4.5e-25	-0.09	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1418	lmev	C	432	543	6e-23	-0.01	0.53		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1418	lmev	C	461	575	1.2e-21	-0.31	0.06		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1418	lsp1		522	547	1.2e-06	-0.44	0.25		SP1F3; CHAIN: NULL;	ZINC FINGER TRANSCRIPTION FACTOR SP1; ZINC FINGER, TRANSCRIPTION ACTIVATION, SP1 COMPLEX (TRANSCRIPTION
1418	lubl	C	408	543	1.4e-24	-0.01	0.07		YY1; CHAIN: C; ADENO-	

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1418	1ubd	C	432	575	1e-24	-0.42	0.03		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1418	2adr		461	549	4.5e-14	0.04	0.17		ADRI; CHAIN: NULL;	TRANSCRIPTION REGULATION, TRANSCRIPTION REGULATION, ADRI, ZINC FINGER, NMR
1418	2adr		522	575	1.4e-12	-0.41	0.03		ADRI; CHAIN: NULL;	TRANSCRIPTION REGULATION, TRANSCRIPTION REGULATION, ADRI, ZINC FINGER, NMR
1418	2drp	A	522	577	1.2e-14	-0.69	0.06		COMPLEX(TRANSCRIPTION REGULATION/DNA) TRAMTRACK PROTEIN (TWO ZINC-FINGER PEPTIDE) COMPLEXED WITH 2DRP 3 DNA 2DRP 4	
1418	2gli	A	369	485	3e-20	-0.05	0.47		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1418	2gli	A	404	575	4.5e-33	-0.16	0.25		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										BINDING PROTEIN/DNA)
1419	1aut	L	118	259	3e-15	0.04	0.17		ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE), PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
1419	1dan	L	136	270	1.5e-15			57.15	BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
1419	1dx5	I	136	232	1e-17	0.14	0.24		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
1419	1dx5	I	168	264	1.1e-13	0.33	0.55		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
1419	1ext	A	31	191	3e-16	0.14	-0.11		TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1419	1ext	A	61	243	3e-16			59.06	TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	PROTEIN
1419	1klo		125	298	9e-22	0.05	-0.01		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1419	1klo		29	185	4.5e-26	0.54	-0.01		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1419	1klo		61	247	4.5e-27	0.51	0.23		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1419	1klo		77	234	4.5e-27			78.19	LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1419	1pfx	L	13	128	1.1e-25	0.07	-0.09		FACTOR IXA; CHAIN: C, L _s ; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR)
1419	1pfx	L	205	298	6e-21	-0.04	0.18		FACTOR IXA; CHAIN: C, L _s ; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR)
1419	1pfx	L	38	165	6e-30			67.49	FACTOR IXA; CHAIN: C, L _s ; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR)
1419	1pfx	L	76	223	6e-30	-0.30	0.31		FACTOR IXA; CHAIN: C, L _s ; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR)

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
										CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
1419	1pp2	R	39	169	1.5e-19	0.24	-0.18		HYDROLASE CALCIUM-FREE PHOSPHOLIPASE A=2= (E.C.3.1.1.4) IPP2 4	
1419	1qfk	L	109	216	3e-15	0.11	0.30		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
1419	1qfk	L	145	247	7.5e-15	0.09	-0.06		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
1419	1skz		141	271	3e-15	-0.17	0.98		ANTISTASIN; CHAIN: NULL;	SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS
1419	1skz		66	179	3e-15			55.31	ANTISTASIN; CHAIN: NULL;	SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS
1419	1tpg		156	237	4.5e-20	0.31	0.53		T-PLASMINOGEN ACTIVATOR	PLASMINOGEN ACTIVATION

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									F1-G; 1TPG 7 CHAIN: NULL; 1TPG 8	
1419	1tpg		220	297	4.5e-15	-0.31	0.18		T-PLASMINOGEN ACTIVATOR F1-G; 1TPG 7 CHAIN: NULL; 1TPG 8	PLASMINOGEN ACTIVATION
1419	1tpg		29	109	7.5e-19	0.14	-0.01		T-PLASMINOGEN ACTIVATOR F1-G; 1TPG 7 CHAIN: NULL; 1TPG 8	PLASMINOGEN ACTIVATION
1419	1vap	A	145	273	9e-16	0.02	-0.19		PHOSPHOLIPASE A2; CHAIN: A, B;	LIPID DEGRADATION PHOSPHOLIPASE A2, LIPID DEGRADATION, HYDROLASE
1419	1vap	A	81	236	7.5e-16	0.04	-0.19		PHOSPHOLIPASE A2; CHAIN: A, B;	LIPID DEGRADATION PHOSPHOLIPASE A2, LIPID DEGRADATION, HYDROLASE
1419	1vpi		81	204	3e-19	0.07	-0.18		PHOSPHOLIPASE A2 INHIBITOR; CHAIN: NULL	NEUROTOXIN PHOSPHOLIPASE A2 INHIBITOR, X-RAY STRUCTURE, RECOGNITION, 2 MOLECULAR EVOLUTION, NEUROTOXIN
1419	1xka	L	145	222	9e-14	0.17	0.37		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
1419	9wga	A	13	142	1.5e-24	0.23	0.30		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9W/GA 3	
1421	1amo	A	272	539	6.8e-40	-0.16	0.01		NADPH-CYTOCHROME P450 REDUCTASE; CHAIN: A, B;	OXIDOREDUCTASE CPR, P450R; X-RAY CRYSTALLOGRAPHY, FLAVOPROTEIN, NITRIC OXIDE SYNTHASE, 2 OXIDOREDUCTASE
1421	1f63	A	252	538	5.1e-57	-0.13	0.21		CHLOROPLAST FERREDOXIN-NADP+ OXIDOREDUCTASE; CHAIN: A, B;	OXIDOREDUCTASE TWO DOMAIN MOTIF, ROSSMANN FOLD

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1421	1fnb		252	538	3.4e-55	0.09	0.01		OXIDOREDUCTASE (NADP+(A), FERREDOXIN(A)) FERREDOXIN:NADP+ OXIDOREDUCTASE (FERREDOXIN REDUCTASE, 1FNB 3 FLAVOENZYME) (E.C.1.1.8.1.2) 1FNB 4 1FNB 72	
1421	1qfj	A	246	510	3.4e-31	-0.07	0.07		FLAVIN REDUCTASE; CHAIN: A, B, C, D;	OXIDOREDUCTASE RIBOFLAVIN, FLAVIN REDUCTASE, FERREDOXIN REDUCTASE 2 SUPERFAMILY, OXIDOREDUCTASE
1421	1qfz	A	252	537	1.7e-54	-0.14	0.43		FERREDOXIN:NADP+ REDUCTASE; CHAIN: A, B;	OXIDOREDUCTASE FNR; FLAVOENZYME, PHOTOSYNTHESIS, ELECTRON TRANSFER, HYDRIDE 2 TRANSFER, OXIDOREDUCTASE
1421	lque		258	538	3.4e-49	0.06	-0.03		FERREDOXIN-NADP+ REDUCTASE; CHAIN: NULL;	OXIDOREDUCTASE FNR; OXIDOREDUCTASE, FLAVOPROTEIN, NADP, FAD, THYLAKOID MEMBRANE, 2 HYCOBILISOME, FNR, NADP+ REDUCTASE
1421	2cnd		244	502	3.4e-57	0.00	-0.12		OXIDOREDUCTASE (NITROGENOUS ACCEPTOR) NADH-DEPENDENT NITRATE REDUCTASE (CYTOCHROME B REDUCTASE 2CND 3 FRAGMENT) (E.C.1.6.6.1) COMPLEXED WITH FAD 2CND 4 (SYNCHROTRON X-RAY DIFFRACTION) 2CND 5	
1426	1alh	A	265	347	1.5e-45			80.07	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA)

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	ZINC FINGER, DNA-BINDING PROTEIN
1426	1mey	C	236	318	1e-51			103.77	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1426	1tff	A	236	402	1.7e-38			99.56	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1426	1ubd	C	211	318	6e-54			88.81	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1426	2gli	A	207	347	6e-69			93.51	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI1; ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1434	1bg1	A	191	320	0.00034	0.41	0.27		STAT3B; CHAIN: A; 18-MER DESOXYOLIGONUCLEOTIDE; CHAIN: B;	COMPLEX (TRANSCRIPTION FACTOR/DNA) TRANSCRIPTION FACTOR, PROTEIN-DNA COMPLEX, CYTOKINE 2 ACTIVATION, COMPLEX (TRANSCRIPTION FACTOR/DNA)
1434	1bz4	A	187	304	1.7e-05	0.25	0.13		APOLIPOPROTEIN E; CHAIN: A;	LIPID BINDING PROTEIN APO-E3;

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	PsiBlast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										LIPID TRANSPORT, LIPID TRANSPORT, HEPARIN-BINDING, PLASMA 2 PROTEIN, HDL, VLDL REMARK
1434	1cii		1	514	1.5e-27			115.08	COLICIN 1A; CHAIN: NULL;	TRANSMEMBRANE PROTEIN COLICIN, BACTERIOCIN, ION CHANNEL FORMATION, TRANSMEMBRANE 2 PROTEIN
1434	1cun	A	127	372	7.5e-11	0.07	-0.01		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1434	1cun	A	228	430	3e-10	0.28	0.00		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1434	1cun	A	253	475	3e-11	0.10	0.10		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1434	1cun	A	389	494	6e-06	0.40	0.40		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1434	1dn1	B	296	481	6e-11	0.05	0.18		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
1434	1ez3	A	316	449	1.5e-08	0.18	-0.18		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1434	1ez3	A	364	486	1.5e-08	0.36	-0.02		SYNTAXIN-1A; CHAIN: A, B, C;	BUNDLE ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
1434	1qsa	A	2	514	3e-20			104.88	SOLUBLE LYTIC TRANSGLYCOSYLASE SLT70; CHAIN: A;	TRANSFERASE ALPHA- SUPERHELIX, TRANSFERASE
1434	1quu	A	228	464	1.5e-18	0.21	0.27		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE- HELIX COILED COIL, CONTRACTILE PROTEIN
1434	1quu	A	332	481	1.2e-09	0.25	-0.17		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE- HELIX COILED COIL, CONTRACTILE PROTEIN
1434	1sig		225	512	3e-09			89.88	RNA POLYMERASE PRIMARY SIGMA FACTOR; CHAIN: NULL;	TRANSCRIPTION REGULATION SIGMA70; RNA POLYMERASE SIGMA FACTOR, TRANSCRIPTION REGULATION
1434	1sig		293	514	3e-09	0.14	0.21		RNA POLYMERASE PRIMARY SIGMA FACTOR; CHAIN: NULL;	TRANSCRIPTION REGULATION SIGMA70; RNA POLYMERASE SIGMA FACTOR, TRANSCRIPTION REGULATION
1437	1rgp		1126	1315	1.5e-53			105.03	RHOGAP; CHAIN: NULL;	G-PROTEIN CDC42 GTPASE- ACTIVATING PROTEIN; G-PROTEIN, GAP, SIGNAL-TRANSDUCTION
1437	1tx4	A	1129	1329	4.5e-58			106.55	P50-RHOGAP; CHAIN: A; TRANSFORMING PROTEIN RHOA; CHAIN: B;	COMPLEX(GTPASE ACTIVATIN/PROTO-ONCOGENE) GTPASE-ACTIVATING PROTEIN RHOGAP; COMPLEX (GTPASE ACTIVATION/PROTO-ONCOGENE), GTPASE, 2 TRANSITION STATE, GAP
1441	1ann		7	299	0			431.20	ANNEXIN IV; 1ANN 5 CHAIN:	CALCIUM/PHOSPHOLIPID-BINDING

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									NULL; 1ANN 6	PROTEIN 32.5 KD CALELECTRIN, ENDONEXIN I; 1ANN 7 32.5KD CALELECTRIN, ENDONEXIN I, LIPOCORTIN IV, 1ANN 12 2 CHROMOBINDIN IV, PROTEIN II 1ANN 13
1447	1dhr		9	213	6.8e-55			304.31	OXIDOREDUCTASE(ACTING ON NADH OR NADPH) DIHYDROPTERIDINE REDUCTASE (DHPR) (E.C.1.6.99.10) COMPLEX 1DHR 3 WITH NADH 1DHR 4	
1452	1b7f	A	1	151	3.4e-33	0.38	0.54		SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'- R(P*GP*UP*UP*GP*UP*UP*UP*UP*UP*UP*U)- CHAIN: P, Q; UP*UP*UP*UP*UP*U)- CHAIN: P, Q;	RNA-BINDING PROTEIN/RNA TRA PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA COMPLEX
1452	1b7f	A	73	230	6.8e-21	0.38	0.99		SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'- R(P*GP*UP*UP*GP*UP*UP*UP*UP*UP*UP*U)- CHAIN: P, Q; UP*UP*UP*UP*UP*U)- CHAIN: P, Q;	RNA-BINDING PROTEIN/RNA TRA PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA COMPLEX
1452	1b7f	A	73	252	6.8e-21			51.11	SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'- R(P*GP*UP*UP*GP*UP*UP*UP*UP*UP*UP*U)- CHAIN: P, Q; UP*UP*UP*UP*UP*U)- CHAIN: P, Q;	RNA-BINDING PROTEIN/RNA TRA PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA COMPLEX
1452	1cvj	A	1	156	3.4e-46			52.06	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1452	1cvj	A	5	157	3.4e-46	0.27	0.80		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D,	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1452	levj	A	77	256	5.1e-24	0.02	0.31		E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1452	levj	B	5	137	6.8e-40	0.25	0.59		POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN I, PABP I; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1452	levj	B	77	230	1.7e-21	0.08	0.15		POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN I, PABP I; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1452	levj	F	77	159	1.7e-19	0.74	1.00		POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN I, PABP I; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1452	levj	H	5	130	1.7e-31	-0.03	0.19		POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN I, PABP I; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Coumpound	PDB annotation
1452	1cvj	H	77	159	1.7e-19	0.81	1.00		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PAPB 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1452	1d8z	A	73	153	1.7e-21	0.73	1.00		HU ANTIGEN C; CHAIN: A;	RNA BINDING PROTEIN RNA-BINDING DOMAIN
1452	1ha1		1	151	1.7e-35	0.06	0.07		HNRNP A1; CHAIN: NULL;	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN
1452	1ha1		75	157	1.7e-21	0.87	1.00		HNRNP A1; CHAIN: NULL;	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN
1452	2u2f	A	74	158	3.4e-19			50.59	SPLICING FACTOR U2AF 65 KD SUBUNIT; CHAIN: A;	RNA-BINDING PROTEIN SPLICING, U2 SNRNP, RBD, RNA-BINDING PROTEIN
1452	2up1	A	1	155	1.2e-36	0.28	0.64		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRAINED TELOMETRIC DNA; CHAIN: B;	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1, UPI; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1
1452	3sx1	A	1	144	3.4e-32	0.13	0.04		SEX-LETHAL; CHAIN: A, B, C;	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1452	3sxl	A	76	230	1.4e-20	0.20	0.69		SEX-LETHAL; CHAIN: A, B, C;	DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION
1452	3sxl	A	7	146	3.4e-32			53.30	SEX-LETHAL; CHAIN: A, B, C;	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION
1454	1c0t	A	345	668	3.4e-85	-0.04	0.87		HIV-1 REVERSE TRANSCRIPTASE (A-CHAIN); CHAIN: A; HIV-1 REVERSE TRANSCRIPTASE (B-CHAIN); CHAIN: B;	TRANSFERASE HIV-1 REVERSE TRANSCRIPTASE, AIDS, NON-NUCLEOSIDE INHIBITOR, 2 DRUG DESIGN
1454	1c0t	B	346	668	5.1e-88	-0.17	0.84		HIV-1 REVERSE TRANSCRIPTASE (A-CHAIN); CHAIN: A; HIV-1 REVERSE TRANSCRIPTASE (B-CHAIN); CHAIN: B;	TRANSFERASE HIV-1 REVERSE TRANSCRIPTASE, AIDS, NON-NUCLEOSIDE INHIBITOR, 2 DRUG DESIGN
1454	1c1c	B	345	668	0	-0.09	0.99		HIV-1 REVERSE TRANSCRIPTASE (A-CHAIN); CHAIN: A; HIV-1 REVERSE TRANSCRIPTASE (B-CHAIN); CHAIN: B;	TRANSFERASE HIV-1 REVERSE TRANSCRIPTASE, AIDS, NON-NUCLEOSIDE INHIBITOR, 2 DRUG DESIGN
1454	1c9r	A	341	671	1.7e-91	-0.06	0.99		HIV-1 REVERSE TRANSCRIPTASE (CHAIN A);	TRANSFERASE/IMMUNE SYSTEM/DNA HIV-1 RT; HIV-1 RT;

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SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: A; HIV-1 REVERSE TRANSCRIPTASE (CHAIN B); CHAIN: B; ANTIBODY (LIGHT CHAIN); CHAIN: L; ANTIBODY (HEAVY CHAIN); CHAIN: H; DNA (5'- CHAIN: T; DNA (5'- CHAIN: P;	HIV, REVERSE TRANSCRIPTASE, MET184ILE, 3TC, PROTEIN-DNA 2 COMPLEX, DRUG RESISTANCE, M184I, TRANSFERASE/IMMUNE 3 SYSTEM/DNA
1454	1c9r	B	341	668	8.5e-98	-0.13	0.99		HIV-1 REVERSE TRANSCRIPTASE (CHAIN A); CHAIN: A; HIV-1 REVERSE TRANSCRIPTASE (CHAIN B); CHAIN: B; ANTIBODY (LIGHT CHAIN); CHAIN: L; ANTIBODY (HEAVY CHAIN); CHAIN: H; DNA (5'- CHAIN: T; DNA (5'- CHAIN: P;	TRANSFERASE/IMMUNE SYSTEM/DNA HIV-1 RT; HIV-1 RT; HIV, REVERSE TRANSCRIPTASE, MET184ILE, 3TC, PROTEIN-DNA 2 COMPLEX, DRUG RESISTANCE, M184I, TRANSFERASE/IMMUNE 3 SYSTEM/DNA
1454	1har		341	551	3.4e-65	0.05	1.00		REVERSE TRANSCRIPTASE HIV-1 REVERSE TRANSCRIPTASE (AMINO-TERMINAL HALF) (FINGERS IHAR 3 AND PALM SUBDOMAINS) (RT216) (E.C.2.7.7.49) IHAR 4	
1454	1mml		326	570	1e-59	0.36	1.00		MMLV REVERSE TRANSCRIPTASE; 1MML 4 CHAIN: NULL; 1MML 5	REVERSE TRANSCRIPTASE
1454	1mml		326	571	1e-59			199.34	MMLV REVERSE TRANSCRIPTASE; 1MML 4 CHAIN: NULL; 1MML 5	REVERSE TRANSCRIPTASE
1454	1rth	A	341	668	0	0.00	1.00		HIV-1 REVERSE TRANSCRIPTASE; 1RTH 4 CHAIN: A, B; 1RTH 5	NUCLEOTIDYLTRANSFERASE HIV-1 RT; 1RTH 6 HIV-1 REVERSE TRANSCRIPTASE 1RTH 15
1454	1rth	B	345	668	0	-0.17	1.00		HIV-1 REVERSE TRANSCRIPTASE; 1RTH 4	NUCLEOTIDYLTRANSFERASE HIV-1 RT; 1RTH 6 HIV-1 REVERSE

SEQ ID NO:	PDB ID	CHAIN N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1454	1vrt	A	345	668	0	-0.04	1.00		CHAIN: A, B; 1RTH 5 HIV-1 REVERSE TRANSCRIPTASE; 1VRT 4 CHAIN: A, B; 1VRT 5	TRANSCRIPTASE 1RTH 15 NUCLEOTIDYLTRANSFERASE HIV-1 RT; 1VRT 6 HIV-1 REVERSE TRANSCRIPTASE 1VRT 15
1454	1vrt	B	345	668	0	-0.09	1.00		HIV-1 REVERSE TRANSCRIPTASE; 1VRT 4 CHAIN: A, B; 1VRT 5	NUCLEOTIDYLTRANSFERASE HIV-1 RT; 1VRT 6 HIV-1 REVERSE TRANSCRIPTASE 1VRT 15
1454	3hvt	B	342	668	3.4e-100	-0.11	0.66		NUCLEOTIDYLTRANSFERASE REVERSE TRANSCRIPTASE (E.C.2.7.7.49) 3HVT 3	
1454	3hvt	B	342	672	3.4e-100			84.10	NUCLEOTIDYLTRANSFERASE REVERSE TRANSCRIPTASE (E.C.2.7.7.49) 3HVT 3	
1455	1dus	A	6	135	5.1e-13	-0.00	-0.08		MJ0882; CHAIN: A;	STRUCTURAL GENOMICS HYPOTHETICAL PROTEIN, METHANOCOCCUS JANNASCHII
1456	ligl		25	94	6.8e-25	0.37	1.00		GROWTH FACTOR INSULIN- LIKE GROWTH FACTOR II (IGF- II, IGF-2) IIGL 3 (NMR, 20 STRUCTURES) IIGL 4 IIGL 78	
1456	ligl		25	94	6.8e-25			108.25	GROWTH FACTOR INSULIN- LIKE GROWTH FACTOR II (IGF- II, IGF-2) IIGL 3 (NMR, 20 STRUCTURES) IIGL 4 IIGL 78	
1456	3lri	A	16	93	4.5e-25	-0.15	1.00		INSULIN-LIKE GROWTH FACTOR I; CHAIN: A;	GROWTH FACTOR INSULIN-LIKE GROWTH FACTOR-I, GROWTH FACTOR, NMR, PROTEIN 2 STRUCTURE, DISTANCE GEOMETRY
1458	2occ	E	46	132	6.8e-37	0.33	1.00		CYTOCHROME C OXIDASE; CHAIN: A, B, C, D, E, F, G, H, I, J,	OXIDOREDUCTASE FERROCYTOCHROME C:OXYGEN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									K, L, M, N, O, P, Q,	OXIDOREDUCTASE; OXIDOREDUCTASE; CYTOCHROME(C)-OXYGEN, CYTOCHROME C 2 OXIDASE
1458	2occ	E	46	132	6.8e-37			115.24	CYTOCHROME C OXIDASE; CHAIN: A, B, C, D, E, F, G, H, I, J, K, L, M, N, O, P, Q,	OXIDOREDUCTASE FERROCYTOCHROME C:OXYGEN OXIDOREDUCTASE; OXIDOREDUCTASE, CYTOCHROME(C)-OXYGEN, CYTOCHROME C 2 OXIDASE
1459	1avs	A	601	640	0.009	0.64	1.00		TROPONIN C; CHAIN: A, B;	MUSCLE CONTRACTION MUSCLE CONTRACTION, CALCIUM- ACTIVATED, TROPONIN, E-F HAND 2 CALCIUM-BINDING PROTEIN
1459	1awj		332	408	3e-11	0.01	0.29		ITK; CHAIN: NULL;	TRANSFERASE IL-2-INDUCIBLE T- CELL KINASE; TRANSFERASE, REGULATORY INTRAMOLECULAR COMPLEX, KINASE
1459	1b8q	A	248	365	1e-18	-0.14	0.87		NEURONAL NITRIC OXIDE SYNTHASE; CHAIN: A; HEPTAPEPTIDE; CHAIN: B;	OXIDOREDUCTASE PDZ DOMAIN, NNOS, NITRIC OXIDE SYNTHASE
1459	1be9	A	248	341	3.4e-16	0.28	0.92		PSD-95; CHAIN: A; CRIP1; CHAIN: B;	PEPTIDE RECOGNITION PEPTIDE RECOGNITION, PROTEIN LOCALIZATION
1459	1g2b	A	334	392	3e-12	-0.25	0.54		SPECTRIN ALPHA CHAIN; CHAIN: A;	METAL BINDING PROTEIN CAPPING PROTEIN, CALCIUM-BINDING, DUPLICATION, REPEAT, SH3 2 DOMAIN, CYTOSKELETON
1459	1gbr	A	340	408	4.5e-11	-0.16	0.13		SIGNAL TRANSDUCTION PROTEIN GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (GRB2, N-TERMINAL 1GBR 3 SH3 DOMAIN) COMPLEXED	

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									WITH SOS-A PEPTIDE 1GBR 4 (NMR, 29 STRUCTURES) 1GBR 5	
1459	1gfc		349	408	1e-10	0.36	0.66		ADAPTOR PROTEIN CONTAINING SH2 AND SH3 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (GRB2) 1GFC 3 (C-TERMINAL SH3 DOMAIN) (NMR, MINIMIZED MEAN STRUCTURE) 1GFC 4	
1459	1gky		479	663	1e-68			146.00	TRANSFERASE GUANYLATE KINASE (E.C.2.7.4.8) COMPLEX WITH 1GKY 3 GUANOSINE MONOPHOSPHATE 1GKY 4	
1459	1gky		480	662	1e-68	0.80	1.00		TRANSFERASE GUANYLATE KINASE (E.C.2.7.4.8) COMPLEX WITH 1GKY 3 GUANOSINE MONOPHOSPHATE 1GKY 4	
1459	1il6		253	345	1.1e-16	0.31	0.95		INTERLEUKIN 16; CHAIN: NULL;	CYTOKINE LCF; CYTOKINE, LYMPHOCYTE CHEMOATTRACTANT FACTOR, PDZ DOMAIN
1459	1kwa	A	254	337	3e-17	0.19	1.00		HCASK/LIN-2 PROTEIN; CHAIN: A, B;	KINASE HCASK, GLGF REPEAT, DHR; PDZ DOMAIN, NEUREXIN, SYNDECAN, RECEPTOR CLUSTERING, KINASE
1459	1kwa	A	257	338	3.4e-16	0.07	0.98		HCASK/LIN-2 PROTEIN; CHAIN: A, B;	KINASE HCASK, GLGF REPEAT, DHR; PDZ DOMAIN, NEUREXIN, SYNDECAN, RECEPTOR CLUSTERING, KINASE
1459	1pdr		253	342	3.4e-14	0.19	0.96		HUMAN DISCS LARGE PROTEIN; CHAIN: NULL;	SIGNAL TRANSDUCTION HDLG, DHR3 DOMAIN; SIGNAL TRANSDUCTION, SH3 DOMAIN, REPEAT

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1459	1pwt		347	408	4.5e-11	0.46	0.58		ALPHA SPECTRIN; CHAIN: NULL;	CIRCULAR PERMUTANT PWT; CIRCULAR PERMUTANT, SH3 DOMAIN, CYTOSKELETON
1459	1qau	A	254	362	1.5e-17	0.13	0.98		NEURONAL NITRIC OXIDE SYNTHASE (RESIDUES 1-130); CHAIN: A;	OXIDOREDUCTASE BETA-FINGER
1459	1qav	A	250	336	4.5e-16	0.24	1.00		ALPHA-1 SYNTROPHIN (RESIDUES 77-171); CHAIN: A; NEURONAL NITRIC OXIDE SYNTHASE (RESIDUES 1-130); CHAIN: B;	MEMBRANE PROTEIN/OXIDOREDUCTASE BETA-FINGER, HETERODIMER
1459	1qkw	A	350	408	3e-11	0.10	0.48		ALPHA II SPECTRIN; CHAIN: A;	CYTOSKELETON CYTOSKELETON, MEMBRANE, SH3 DOMAIN
1459	1qly	A	349	408	1.3e-10	0.41	0.47		TYROSINE-PROTEIN KINASE BTK; CHAIN: A;	TYROSINE-PROTEIN KINASE BRUTONS TYROSINE KINASE, B CELL PROGENITOR KINASE, TRANSFERASE, TYROSINE-PROTEIN KINASE, PHOSPHORYLATION, 2 SH3 DOMAIN
1459	1sem	A	350	408	1.5e-10	-0.10	0.41		SEM-5; 1SEM 3 CHAIN: A, B; 1SEM 5 10-RESIDUE PROLINE-RICH PEPTIDE FROM MSOS 1SEM 8 CHAIN: C, D 1SEM 10	SIGNAL TRANSDUCTION PROTEIN SRC-HOMOLOGY 3 (SH3) DOMAIN, PEPTIDE-BINDING PROTEIN, 1SEM 18 2 GUANINE NUCLEOTIDE EXCHANGE FACTOR 1SEM 19
1459	1tud		334	392	6e-13	0.22	0.40		ALPHA-SPECTRIN; CHAIN: NULL;	CYTOSKELETON CAPPING PROTEIN, CALCIUM-BINDING, DUPLICATION, REPEAT, 2 SH3 DOMAIN, CYTOSKELETON
1459	1ukz		477	659	1.4e-07	0.10	0.69		TRANSFERASE URIDYLATE KINASE (E.C.2.7.4.-) COMPLEXED WITH ADP AND AMP 1UKZ 3.	
1459	1zak	A	482	662	1.2e-05	0.02	0.22		ADENYLATE KINASE; CHAIN:	TRANSFERASE ATP:AMP-

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Coumpound	PDB annotation
									A, B;	PHOSPHOTRANSFERASE, TRANSFERASE
1459	3adk		475	662	9e-06	0.12	0.98		TRANSFERASE(PHOSPHOTRANSFERASE) ADENYLATE KINASE (E.C.2.7.4.3) 3ADK 4	
1459	3pdz	A	253	332	1.5e-13	0.32	1.00		TYROSINE PHOSPHATASE (PTP-BAS, TYPE 1); CHAIN: A;	HYDROLASE PDZ DOMAIN, HUMAN PHOSPHATASE, HPTP1E, PTP-BAS, SPECIFICITY 2 OF BINDING
1459	3tmk	C	479	662	9e-10	0.28	0.04		THYMIDYLATE KINASE; CHAIN: A, B, C, D, E, F, G, H;	KINASE KINASE, PHOSPHOTRANSFERASE
1459	4tmk	A	478	662	7.5e-16	-0.03	0.19		THYMIDYLATE KINASE; CHAIN: A;	TRANSFERASE ATP-DTMP PHOSPHOTRANSFERASE
1461	1bg3	A	1	498	0	1.13	1.00		HEXOKINASE; CHAIN: A, B;	HEXOKINASE ATP/D-HEXOSE-6-PHOSPHOTRANSFERASE; HEXOKINASE, PHOSPHOTRANSFERASE
1461	1bg3	A	1	499	0			459.01	HEXOKINASE; CHAIN: A, B;	HEXOKINASE ATP/D-HEXOSE-6-PHOSPHOTRANSFERASE; HEXOKINASE, PHOSPHOTRANSFERASE
1461	1cza	N	1	501	0	1.07	1.00		HEXOKINASE TYPE I; CHAIN: N;	TRANSFERASE STRUCTURALLY HOMOLOGOUS DOMAINS
1464	1a0j	A	30	239	1.4e-80	0.88	1.00		TRYPSIN; CHAIN: A, B, C, D;	SERINE PROTEASE SERINE PROTEINASE, TRYPSIN, HYDROLASE
1464	1a0j	A	30	239	1.4e-80			104.84	TRYPSIN; CHAIN: A, B, C, D;	SERINE PROTEASE SERINE PROTEINASE, TRYPSIN, HYDROLASE
1464	1a0l	A	30	233	1.7e-74	0.50	1.00		BETA-TRYPTASE; CHAIN: A, B, C, D;	SERINE PROTEINASE TRYPSIN-LIKE SERINE PROTEINASE, TETRAMER, HEPARIN, ALLERGY, 2 ASTHMA
1464	1a0l	A	30	239	1.7e-74			97.00	BETA-TRYPTASE; CHAIN: A, B,	SERINE PROTEINASE TRYPSIN-LIKE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									C, D;	SERINE PROTEINASE, TETRAMER, HEPARIN, ALLERGY, 2 ASTHMA
1464	1bru	P	30	239	1.7e-75	0.64	1.00		ELASTASE; CHAIN: P;	SERINE PROTEASE PPE; SERINE PROTEASE, HYDROLASE
1464	1bru	P	30	239	1.7e-75			115.93	ELASTASE; CHAIN: P;	SERINE PROTEASE PPE; SERINE PROTEASE, HYDROLASE
1464	1dpo		30	239	1.7e-79			98.94	TRYPSIN; CHAIN: NULL;	SERINE PROTEASE HYDROLASE, SERINE PROTEASE, DIGESTION, PANCREAS, ZYMOGEN, 2 SIGNAL, MULTIGENE FAMILY
1464	1fuj	A	30	237	6e-71			200.42	PR3; CHAIN: A, B, C, D;	HYDROLASE (SERINE PROTEASE) MYELOBLASTIN; HYDROLASE, SERINE PROTEASE, GLYCOPROTEIN, ZYMOGEN, SIGNAL
1464	1mct	A	30	239	8.5e-83	0.74	1.00		COMPLEX(PROTEINASE/INHIBITOR) TRYPSIN (E.C.3.4.21.4) COMPLEXED WITH INHIBITOR FROM BITTER 1MCT 3 GOURD 1MCT 4	
1464	1mct	A	30	239	8.5e-83			103.86	COMPLEX(PROTEINASE/INHIBITOR) TRYPSIN (E.C.3.4.21.4) COMPLEXED WITH INHIBITOR FROM BITTER 1MCT 3 GOURD 1MCT 4	
1464	1ppf	E	30	237	1e-65			315.52	HYDROLASE(SERINE PROTEINASE) HUMAN LEUKOCYTE ELASTASE (HLE) (NEUTROPHIL ELASTASE (HNE)) 1PPF 3 (E.C.3.4.21.37) COMPLEX WITH THE THIRD DOMAIN OF TURKEY 1PPF 4 OVOMUCOID INHIBITOR (OMTKY3) 1PPF 5	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1464	1qrz	A	12	239	3.4e-71			117.30	PLASMINOGEN; CHAIN: A, B, C, D;	HYDROLASE MICROPLASMINOGEN, SERINE PROTEASE, ZYMOGEN, CHYMOTRYPSIN 2 FAMILY, HYDROLASE
1464	1sgf	G	30	239	3.4e-72	0.65	1.00		NERVE GROWTH FACTOR; CHAIN: A, B, G, X, Y, Z;	GROWTH FACTOR 7S NGF; GROWTH FACTOR (BETA-NGF), HYDROLASE - SERINE PROTEINASE 2 (GAMMA-NGF), INACTIVE SERINE PROTEINASE (ALPHA-NGF)
1464	1sgf	G	30	240	3.4e-72			97.78	NERVE GROWTH FACTOR; CHAIN: A, B, G, X, Y, Z;	GROWTH FACTOR 7S NGF; GROWTH FACTOR (BETA-NGF), HYDROLASE - SERINE PROTEINASE 2 (GAMMA-NGF), INACTIVE SERINE PROTEINASE (ALPHA-NGF)
1464	1slw	B	30	239	1.7e-78	0.45	1.00		ECOTIN; CHAIN: A; ANIONIC TRYPSIN; CHAIN: B;	COMPLEX (SERINE PROTEASE/INHIBITOR) TRYPSIN INHIBITOR; SERINE PROTEASE, INHIBITOR, COMPLEX, METAL BINDING SITES, 2 PROTEIN ENGINEERING, PROTEASE- SUBSTRATE INTERACTIONS, 3 METALLOPROTEINS
1464	1tm	A	30	239	5.1e-80	0.79	1.00		HYDROLASE (SERINE PROTEINASE) TRYPSIN (E.C.3.4.21.4) COMPLEXED WITH THE INHIBITOR ITRN 3 DIISOPROPYL- FLUOROPHOSPHORODIAT E (DFP) ITRN 4 HUMAN TRYPSIN, DFP INHIBITED ITRN 6	
1464	1tm	A	30	240	5.1e-80			100.94	HYDROLASE (SERINE PROTEINASE) TRYPSIN	

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									(E.C.3.4.21.4) COMPLEXED WITH THE INHIBITOR ITRN 3 DIISOPROPYL-FLUOROPHOSPHORIDAT E (DFP) ITRN 4 HUMAN TRYPSIN, DFP INHIBITED ITRN 6	
1464	2tbs		30	237	5.1e-79	0.65	1.00		HYDROLASE(SERINE PROTEINASE) TRYPSIN (E.C.3.4.21.4) COMPLEXED WITH BENZAMIDINE INHIBITOR 2TBS 3	
1464	2tbs		30	239	5.1e-79			97.32	HYDROLASE(SERINE PROTEINASE) TRYPSIN (E.C.3.4.21.4) COMPLEXED WITH BENZAMIDINE INHIBITOR 2TBS 3	
1464	5ptp		30	239	1.7e-76	0.73	1.00		BETA TRYPSIN; CHAIN: NULL;	SERINE PROTEASE HYDROLASE, SERINE PROTEASE, DIGESTION, PANCREAS, 2 ZYMOGEN, SIGNAL
1464	5ptp		30	239	1.7e-76			99.14	BETA TRYPSIN; CHAIN: NULL;	SERINE PROTEASE HYDROLASE, SERINE PROTEASE, DIGESTION, PANCREAS, 2 ZYMOGEN, SIGNAL
1470	1a4o	A	3	229	1.7e-98			234.97	14-3-3 PROTEIN ZETA; CHAIN: A, B, C, D;	SIGNAL TRANSDUCTION SIGNAL TRANSDUCTION
1470	1a4o	A	3	230	1.7e-98	0.55	1.00		14-3-3 PROTEIN ZETA; CHAIN: A, B, C, D;	SIGNAL TRANSDUCTION SIGNAL TRANSDUCTION
1470	1qja	A	3	232	0	0.59	1.00		14-3-3 PROTEIN ZETA; CHAIN: A, B; PHOSPHOPEPTIDE; CHAIN: Q, R	COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE) COMPLEX, 14-3-3, PHOSPHOPEPTIDE, SIGNAL TRANSDUCTION
1470	1qja	A	3	232	0			284.35	14-3-3 PROTEIN ZETA; CHAIN:	COMPLEX (SIGNAL

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									A, B; PHOSPHOPEPTIDE; CHAIN: Q, R	TRANSDUCTION/PEPTIDE) COMPLEX, 14-3-3, PHOSPHOPEPTIDE, SIGNAL TRANSDUCTION
1471	1cii		48	621	3.4e-08			133.38	COLICIN 1A; CHAIN: NULL;	TRANSMEMBRANE PROTEIN COLICIN, BACTERIOCIN, ION CHANNEL FORMATION, TRANSMEMBRANE 2 PROTEIN
1471	1cun	A	117	322	6e-15	-0.15	0.03		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1471	1cun	A	152	363	7.5e-16	0.12	-0.17		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1471	1cun	A	38	248	3e-20	0.05	0.39		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1471	1ez3	A	23	139	1.5e-09	0.19	-0.13		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
1471	1ez3	A	95	214	4.5e-08	0.01	-0.15		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
1471	1quu	A	196	426	6e-19	0.02	0.11		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1471	1quu	A	217	487	1.5e-15	0.09	-0.02		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
1471	1sig		32	307	6e-09	-0.11	0.03		RNA POLYMERASE PRIMARY SIGMA FACTOR; CHAIN: NULL;	TRANSCRIPTION REGULATION SIGMA70; RNA POLYMERASE SIGMA FACTOR, TRANSCRIPTION REGULATION
1475	1nfi	E	23	77	0.0045	-0.56	0.04		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1476	1cun	A	150	337	3e-06	-0.18	0.15		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1476	1cun	A	241	458	9e-13	-0.12	0.19		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1476	1cun	A	460	687	1.5e-15	-0.05	0.55		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1476	1cun	A	506	724	4.5e-15	0.19	0.35		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1476	1cun	A	583	794	9e-17	0.15	0.42		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN
1476	1cun	A	632	850	1.2e-13	0.08	0.09		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1476	1cun	A	721	916	6e-12	-0.00	-0.14		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1476	1dn1	B	216	423	6e-16	0.03	-0.05		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
1476	1dn1	B	380	597	1.5e-16	-0.30	0.01		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
1476	1dn1	B	503	711	6e-18	-0.21	0.06		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
1476	1dn1	B	700	911	6e-13	-0.19	0.03		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
1476	1ez3	A	256	363	3e-07	-0.26	0.03		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
1476	1ez3	A	593	719	1.5e-11	0.00	-0.06		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										KDA PROTEIN, P35A, THREE HELIX BUNDLE
1476	1ez3	A	704	822	4.5e-10	0.28	0.19		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
1476	1fio	A	491	648	9e-10	0.17	0.15		SSO1 PROTEIN; CHAIN: A;	MEMBRANE PROTEIN FOUR HELIX BUNDLE, ALPHA HELIX
1476	1fxk	C	548	711	0.0001	-0.29	0.59		PREFOLDIN; CHAIN: A; PREFOLDIN; CHAIN: B; PREFOLDIN; CHAIN: C;	CHAPERONE ARCHAEAL PROTEIN
1476	1quu	A	320	573	4.5e-22	-0.19	0.00		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
1476	1quu	A	390	640	3e-26	-0.29	0.06		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
1476	1quu	A	480	749	6e-24	-0.02	0.54		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
1476	1quu	A	528	790	1.5e-24	0.07	0.21		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
1476	1ses	A	464	555	0.00017	-0.07	0.12		LIGASE(SYNTHETASE) SERYL-TRNA SYNTHETASE (E.C.6.1.1.11) (SERINE-TRNA LIGASE) 1SES 3 COMPLEXED WITH SERYL-HYDROXAMATE-AMP 1SES 4	
1479	1dl4	A	609	667	0.00015	0.62	0.82		NEURO-ONCOLOGICAL VENTRAL ANTIGEN 1; CHAIN: A;	IMMUNE SYSTEM KH DOMAIN, ALPHA-BETA FOLD, RNA-BINDING MOTIF
1479	1dtj	A	609	667	0.00075	0.19	0.96		RNA-BINDING	IMMUNE SYSTEM KH DOMAIN,

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									NEUROONCOLOGICAL VENTRAL ANTIGEN 2; CHAIN: A, B, C, D;	ALPHA-BETA FOLD RNA-BINDING MOTIF
1479	1dtj	C	609	667	3e-06	0.59	0.94		RNA-BINDING NEUROONCOLOGICAL VENTRAL ANTIGEN 2; CHAIN: A, B, C, D;	IMMUNE SYSTEM KH DOMAIN, ALPHA-BETA FOLD RNA-BINDING MOTIF
1479	1dtj	D	609	667	1e-05	0.60	0.89		RNA-BINDING NEUROONCOLOGICAL VENTRAL ANTIGEN 2; CHAIN: A, B, C, D;	IMMUNE SYSTEM KH DOMAIN, ALPHA-BETA FOLD RNA-BINDING MOTIF
1479	1e3h	A	51	613	0	0.75	1.00		GUANOSINE PENTAPHOSPHATE SYNTHETASE; CHAIN: A;	POLYRIBONUCLEOTIDE TRANSFERASE POLYNUCLEOTIDE PHOSPHORYLASE, GUANOSINE POLYRIBONUCLEOTIDE TRANSFERASE, ATP:GTP 2 DIPHOSPHOTRANSFERASE, RNA PROCESSING, RNA DEGRADATION
1479	1e3p	A	51	739	0	0.49	1.00		GUANOSINE PENTAPHOSPHATE SYNTHETASE; CHAIN: A;	POLYRIBONUCLEOTIDE TRANSFERASE POLYNUCLEOTIDE PHOSPHORYLASE, GUANOSINE POLYRIBONUCLEOTIDE TRANSFERASE, ATP-GTP DIPHOSPHOTRANSFERASE, 2 RNA PROCESSING, RNA DEGRADATION
1479	1ec6	A	609	675	0.00014	0.50	0.72		RNA-BINDING PROTEIN NOVA-2; CHAIN: A, B; 20-MER RNA HAIRPIN; CHAIN: C, D;	RNA BINDING PROTEIN/RNA ASTROCYTIC NOVA-LIKE RNA-BINDING PROTEIN; KH DOMAIN, ALPHA-BETA FOLD, RNA-BINDING MOTIF, PROTEIN/RNA 2 STRUCTURE
1479	1khn	A	610	671	0.0014	0.36	0.36		HNRNP K; CHAIN: A;	RNA BINDING PROTEIN KH3; HNRNP K, KH DOMAIN, THREE-DIMENSIONAL STRUCTURE, NMR,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1479	1sto		675	751	5.1e-21	0.78	1.00		PNPASE; CHAIN: NULL;	C-MYC, 2 DIPOLAR COUPLING, DNA-BINDING, RNA-BINDING, RNA BINDING 3 PROTEIN
1479	lvig		603	667	1e-06	0.46	0.30		VIGILIN; 1VIG 5 CHAIN: NULL; 1VIG 6	S1 RNA-BINDING DOMAIN POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE, S1 RNA-BINDING DOMAIN, POLYNUCLEOTIDE PHOSPHORYLASE 2 (PNPASE)
1480	1d9x	A	442	528	1.7e-06	-0.14	0.00		EXCINUCLEASE UVRABC COMPONENT UVRB; CHAIN: A;	GENE REGULATION APO PROTEIN
1480	1d9x	A	447	602	0.009	-0.21	0.03		EXCINUCLEASE UVRABC COMPONENT UVRB; CHAIN: A;	GENE REGULATION APO PROTEIN
1480	1fn	A	427	492	0.00015	-0.14	0.54		CELL DIVISION CONTROL PROTEIN 6; CHAIN: A, B;	CELL CYCLE CDC6P; CDC6, CDC18, ORC1, AAA PROTEIN, DNA REPLICATION INITIATION 2 FACTOR, CELL CYCLE CONTROL FACTOR
1480	1qhg	A	444	524	1.5e-11	-0.19	0.83		PCRA (SUBUNIT); CHAIN: A; PCRA (SUBUNIT); CHAIN: B; PCRA (SUBUNIT); CHAIN: C; PCRA (SUBUNIT); CHAIN: D;	HELICASE DNA REPAIR, DNA REPLICATION, SOS RESPONSE, HELICASE, ATP- 2 BINDING, DNA-BINDING
1484	1aoa		4	122	6.8e-26	0.28	0.96		T-FIMBRIN; CHAIN: NULL;	ACTIN-BINDING PROTEIN ACTIN-BINDING PROTEIN, CALCIUM-BINDING, PHOSPHORYLATION
1484	1dxx	A	2	120	5.1e-28	0.54	0.68		DYSTROPHIN; CHAIN: A, B, C, D;	STRUCTURAL PROTEIN DYSTROPHIN, MUSCULAR DYSTROPHY, CALPONIN HOMOLOG DOMAIN, 2 ACTIN-BINDING, UTROPHIN

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1484	1qag	A	5	121	3.4e-26	0.33	0.39		UTROPHIN ACTIN BINDING REGION; CHAIN: A, B;	STRUCTURAL PROTEIN CALPONIN HOMOLOG DOMAIN, DOMAIN SWAPPING, ACTIN BINDING, 2 UTROPHIN, DYSTROPHIN, STRUCTURAL PROTEIN
1486	1tf6	A	866	953	0.0045	-0.10	0.01		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1486	2gli	A	873	926	0.00045	0.08	0.41		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1487	1bor		339	377	0.0001	-0.38	0.00		TRANSCRIPTION FACTOR PML; CHAIN: NULL;	TRANSCRIPTION REGULATION PROTO-ONCOGENE, NUCLEAR BODIES (PODS), LEUKEMIA, 2 TRANSCRIPTION REGULATION
1487	1chc		336	378	3.4e-10	-0.35	0.29		VIRUS EQUINE HERPES VIRUS-1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	
1487	1fbv	A	336	381	5.1e-09	-0.24	0.15		SIGNAL TRANSDUCTION PROTEIN CBL; CHAIN: A; ZAP-70 PEPTIDE; CHAIN: B; UBIQUITIN-CONJUGATING ENZYME E12-18 KDA UBCH7; CHAIN: C;	LIGASE CBL, UBCH7, ZAP-70, E2, UBIQUITIN, E3, PHOSPHORYLATION, 2 TYROSINE KINASE, UBIQUITINATION, PROTEIN DEGRADATION,
1487	1g25	A	336	387	5.1e-06	0.26	0.62		CDK-ACTIVATING KINASE ASSEMBLY FACTOR MAT1;	METAL BINDING PROTEIN RING FINGER PROTEIN MAT1; RING

SEQ ID NO:	PDB ID	CHAI NID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1487	1rmd		320	387	3.4e-09	0.10	0.06		CHAIN: A; RAG1; CHAIN: NULL;	FINGER (C3HC4) DNA-BINDING PROTEIN V(D)J RECOMBINATION ACTIVATING PROTEIN 1; RAG1, V(D)J RECOMBINATION, ANTIBODY, MAD, RING FINGER, 2 ZINC BINUCLEAR CLUSTER, ZINC FINGER, DNA-BINDING PROTEIN
1490	1d2n	A	626	782	1.2e-11	0.11	-0.18		N-ETHYLMALIMIDE- SENSITIVE FUSION PROTEIN; CHAIN: A;	HEXAMERIZATION DOMAIN HEXAMERIZATION DOMAIN, ATPASE, TRANSPORT
1490	1e94	E	339	434	8.5e-12	0.01	-0.13		HEAT SHOCK PROTEIN HSLV; CHAIN: A, B, C, D; HEAT SHOCK PROTEIN HSLU; CHAIN: E, F;	CHAPERONE HSLV; HSLU CHAPERONE, HSLVU, CLPQY, AAA- ATPASE, ATP-DEPENDENT 2 PROTEOLYSIS, PROTEASOME
1490	1e94	E	339	634	1.5e-12	-0.20	0.05		HEAT SHOCK PROTEIN HSLV; CHAIN: A, B, C, D; HEAT SHOCK PROTEIN HSLU; CHAIN: E, F;	CHAPERONE HSLV; HSLU CHAPERONE, HSLVU, CLPQY, AAA- ATPASE, ATP-DEPENDENT 2 PROTEOLYSIS, PROTEASOME
1490	1f48	A	82	514	0.0015	-0.39	0.28		ARSENITE-TRANSLOCATING ATPASE; CHAIN: A;	HYDROLASE ARSA ATPASE; P- LOOP, ANTIMONITE BINDING SITE, ATP BINDING SITE
1490	1fnn	A	344	629	1.2e-15	0.15	0.45		CELL DIVISION CONTROL PROTEIN 6; CHAIN: A, B;	CELL CYCLE CDC6P; CDC6, CDC18, ORC1, AAA PROTEIN, DNA REPLICATION INITIATION 2 FACTOR, CELL CYCLE CONTROL FACTOR
1490	1g41	A	330	599	1.2e-37	0.46	0.94		HEAT SHOCK PROTEIN HSLU; CHAIN: A;	CHAPERONE AAA-ATPASE, CLPY, ATP-DEPENDENT PROTEOLYSIS
1490	1g41	A	339	618	1.2e-17	-0.11	0.04		HEAT SHOCK PROTEIN HSLU; CHAIN: A;	CHAPERONE AAA-ATPASE, CLPY, ATP-DEPENDENT PROTEOLYSIS
1490	1shk	A	369	396	1.5e-05	-0.53	0.49		SHIKIMATE KINASE; CHAIN: A, B;	TRANSFERASE SHIKIMATE KINASE, PHOSPHORYL TRANSFER, ADP,

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1490	2ffh	A	347	537	1e-05	-0.24	0.01		FFH; CHAIN: A, B, C;	SHIKIMATE 2 PATHWAY, P-LOOP PROTEIN, TRANSFERASE PROTEIN TRANSPORT FIFTY-FOUR HOMOLOG, P48; FFH, SRP54, SIGNAL RECOGNITION PARTICLE, GTPASE, M DOMAIN; 2 RNA-BINDING, SIGNAL SEQUENCE-BINDING, HELIX-TURN-HELIX, 3 PROTEIN TARGETING, PROTEIN TRANSPORT
1491	1a4y	A	178	394	1.5e-48	0.10	0.94		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPIPOPE MAPPING, LEUCINE-RICH 3 REPEATS
1491	1yrg	A	178	391	6.8e-27	0.03	0.18		GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	TRANSCRIPTION RNAIP; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPII, GTPASE-ACTIVATING PROTEIN, GAP, RNAIP, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
1491	2bnh		178	393	3.4e-43	0.33	0.65		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1495	1lit		36	166	1e-42	0.82	1.00		LITHOSTATHINE; CHAIN: NULL	PANCREATIC STONE INHIBITOR, PANCREATIC STONE INHIBITOR, LECTIN

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1495	1lit		36	166	7.5e-43	0.82	1.00		LITHOSTATHINE; CHAIN: NULL	PANCREATIC STONE INHIBITOR PANCREATIC STONE INHIBITOR, LECTIN
1495	1lit		36	166	7.5e-43			212.11	LITHOSTATHINE; CHAIN: NULL	PANCREATIC STONE INHIBITOR PANCREATIC STONE INHIBITOR, LECTIN
1495	1qdd	A	23	166	1e-44	0.77	1.00		LITHOSTATHINE; CHAIN: A;	METAL BINDING PROTEIN PANCREATIC STONE PROTEIN, PSP; PANCREATIC STONE INHIBITOR, LITHOSTATHINE
1495	1qdd	A	23	166	6e-47	0.77	1.00		LITHOSTATHINE; CHAIN: A;	METAL BINDING PROTEIN PANCREATIC STONE PROTEIN, PSP; PANCREATIC STONE INHIBITOR, LITHOSTATHINE
1495	1qdd	A	23	166	6e-47			226.04	LITHOSTATHINE; CHAIN: A;	METAL BINDING PROTEIN PANCREATIC STONE PROTEIN, PSP; PANCREATIC STONE INHIBITOR, LITHOSTATHINE
1497	1qqe	A	489	634	1.1e-13	0.14	-0.17		VESICULAR TRANSPORT PROTEIN SEC17; CHAIN: A;	PROTEIN TRANSPORT HELIX- TURN-HELIX TPR-LIKE REPEAT, PROTEIN TRANSPORT
1498	1eul	A	1	713	0	-0.16	0.46		CALCIUM-TRANSPORTING ATPASE SARCOPLASMIC CHAIN: A;	HYDROLASE SERCA1; ION PUMP, CALCIUM, MEMBRANE PROTEIN, P- TYPE ATPASE, ACTIVE 2 TRANSPORT
1499	1c4o	A	393	540	1e-12	0.20	0.96		DNA NUCLEOTIDE EXCISION REPAIR ENZYME UVRB; CHAIN: A;	REPLICATION DNA NUCLEOTIDE EXCISION REPAIR, UVRABC, HELICASE, 2 HYPERTHERMOSTABLE PROTEIN
1499	1c4o	A	448	516	1.4e-19	-0.10	0.83		DNA NUCLEOTIDE EXCISION REPAIR ENZYME UVRB;	REPLICATION DNA NUCLEOTIDE EXCISION REPAIR, UVRABC,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									CHAIN: A;	HELICASE, 2 HYPERTHERMOSTABLE PROTEIN
1499	1d2m	A	144	223	0.00068	-0.57	0.19		EXCINUCLEASE ABC SUBUNIT B; CHAIN: A;	HYDROLASE UVRB; MULTIDOMAIN PROTEIN
1499	1d2m	A	393	540	8.5e-13	0.17	0.80		EXCINUCLEASE ABC SUBUNIT B; CHAIN: A;	HYDROLASE UVRB; MULTIDOMAIN PROTEIN
1499	1d9x	A	238	531	9e-29	-0.16	0.09		EXCINUCLEASE UVRABC COMPONENT UVRB; CHAIN: A;	GENE REGULATION APO PROTEIN
1499	1d9x	A	380	528	3.4e-16	0.39	0.76		EXCINUCLEASE UVRABC COMPONENT UVRB; CHAIN: A;	GENE REGULATION APO PROTEIN
1499	1fuk	A	376	558	1.2e-43	0.26	0.86		EUKARYOTIC INITIATION FACTOR 4A; CHAIN: A;	TRANSLATION YEAST INITIATION FACTOR 4A, EIF4A; HELICASE, INITIATION FACTOR 4A, DEAD-BOX PROTEIN
1499	1fuu	A	127	340	3.4e-59	0.83	1.00		YEAST INITIATION FACTOR 4A; CHAIN: A, B;	TRANSLATION EUKARYOTIC INITIATION FACTOR 4A; IF4A, HELICASE, DEAD-BOX PROTEIN
1499	1fuu	B	127	558	0	0.47	1.00		YEAST INITIATION FACTOR 4A; CHAIN: A, B;	TRANSLATION EUKARYOTIC INITIATION FACTOR 4A; IF4A, HELICASE, DEAD-BOX PROTEIN
1499	1hei	A	158	325	0.0003	-0.18	0.22		HCV HELICASE; CHAIN: A, B;	HELICASE HELICASE, RNA, HEPATITIS, HCV, ATPASE, NTPASE
1499	1qde	A	127	340	5.1e-56	0.55	1.00		TRANSLATION INITIATION FACTOR 4A; CHAIN: A;	GENE REGULATION EIF4A; TRANSLATION INITIATION, SACCHAROMYCES CEREVISIAE, DEAD BOX 2 PROTEIN FAMILY
1499	8ohm		158	522	1.5e-53	-0.59	0.04		RNA HELICASE; CHAIN: NULL	HELICASE RNA HELICASE, HEPATITIS C VIRUS, HCV, UNWINDING MECHANISM
1502	1a25	A	12	137	9e-25			77.04	PROTEIN KINASE C (BETA); CHAIN: A, B;	CALCIUM-BINDING PROTEIN CALB; CALCIUM++/PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM-BINDING PROTEIN

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1502	1a25	A	167	287	1.5e-26	-0.05	0.54		PROTEIN KINASE C (BETA); CHAIN: A, B;	CALCIUM-BINDING PROTEIN CALB; CALCIUM++/PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM-BINDING PROTEIN
1502	1a25	A	17	131	9e-25	0.42	1.00		PROTEIN KINASE C (BETA); CHAIN: A, B;	CALCIUM-BINDING PROTEIN CALB; CALCIUM++/PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM-BINDING PROTEIN
1502	1a25	A	18	117	1.4e-24	0.62	0.90		PROTEIN KINASE C (BETA); CHAIN: A, B;	CALCIUM-BINDING PROTEIN CALB; CALCIUM++/PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM-BINDING PROTEIN
1502	1byn	A	167	287	3.4e-30	0.04	0.35		SYNAPTOTAGMIN I; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS
1502	1byn	A	19	122	1.7e-28	0.36	0.10		SYNAPTOTAGMIN I; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS
1502	1c1y	A	184	338	1.3e-29	0.07	0.65		CYTOSOLIC PHOSPHOLIPASE A2; CHAIN: A, B;	HYDROLASE CPLA2; PHOSPHOLIPASE, LIPID-BINDING, HYDROLASE
1502	1c1y	A	22	184	7.5e-24	0.29	0.45		CYTOSOLIC PHOSPHOLIPASE A2; CHAIN: A, B;	HYDROLASE CPLA2; PHOSPHOLIPASE, LIPID-BINDING, HYDROLASE
1502	1d1x	A	183	302	3.4e-22	0.34	0.24		PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	LIPID DEGRADATION PLC-D1; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1502	1dix	A	27	121	6.8e-23	0.49	0.16		PHOSPHOINOSITIDE-SPECIFIC LIPID DEGRADATION PLC-D1; PHOSPHOLIPASE C, CHAIN: A, B;	PHOSPHOINOSITIDE-SPECIFIC LIPID DEGRADATION PLC-D1; PHOSPHOLIPASE C, CHAIN: A, B; HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3 PHOSPHOINOSITIDE-SPECIFIC
1502	1dix	B	183	302	3.4e-22	0.20	0.21		PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	PHOSPHOINOSITIDE-SPECIFIC LIPID DEGRADATION PLC-D1; PHOSPHOLIPASE C, CHAIN: A, B; HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3 PHOSPHOINOSITIDE-SPECIFIC
1502	1dsy	A	17	137	1e-24	0.52	1.00		PROTEIN KINASE C, ALPHA TYPE; CHAIN: A;	TRANSFERASE CALCIUM++, PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYL SERINE, PROTEIN KINASE C
1502	1dsy	A	183	295	5.1e-28	-0.13	0.07		PROTEIN KINASE C, ALPHA TYPE; CHAIN: A;	TRANSFERASE CALCIUM++, PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYL SERINE, PROTEIN KINASE C
1502	1dsy	A	18	117	6.8e-27	0.47	0.88		PROTEIN KINASE C, ALPHA TYPE; CHAIN: A;	TRANSFERASE CALCIUM++, PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYL SERINE, PROTEIN KINASE C
1502	1rlw		184	276	6e-23	0.17	0.28		PHOSPHOLIPASE A2; CHAIN: NULL;	HYDROLASE CALB DOMAIN; HYDROLASE, C2 DOMAIN, CALB DOMAIN
1502	1rlw		20	145	4.5e-25			51.76	PHOSPHOLIPASE A2; CHAIN:	HYDROLASE CALB DOMAIN;

SEQ ID NO:	PDB ID	CHAI NID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									NULL;	HYDROLASE, C2 DOMAIN, CALB DOMAIN
1502	1rlw		30	143	4.5e-25	0.78	0.93		PHOSPHOLIPASE A2; CHAIN: NULL;	HYDROLASE CALB DOMAIN; HYDROLASE, C2 DOMAIN, CALB DOMAIN
1502	1rsy		167	284	3.4e-30	0.18	0.48		CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3	
1502	1rsy		19	122	1.7e-28	0.36	0.21		CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3	
1502	1rsy		2	130	1.7e-28			59.11	CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3	
1502	3rpb	A	168	294	1.2e-26	0.00	0.34		RABPHILIN 3-A; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS C2-DOMAINS, C2B-DOMAIN, RABPHILIN, ENDOCYTOSIS/EXOCYTOSIS
1502			144	223	6.8e-53	-0.57	0.19		SYNAPTOTAGMIN III; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS BETA SANDWICH, CALCIUM ION, C2 DOMAIN
1503	lawc	B	693	861	1.5e-26	0.40	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA I; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1503	lawc	B	694	828	1.2e-29	0.29	0.96		GA BINDING PROTEIN ALPHA;	COMPLEX (TRANSCRIPTION

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D; E;	REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1503	1awc	B	748	895	5.1e-38	0.68	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D; E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1503	1awc	B	779	936	7.5e-34	0.72	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D; E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1503	1awc	B	780	970	1.2e-31	0.02	0.78		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D; E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1503	1awc	B	847	1005	3.4e-29	0.08	-0.11		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									DNA; CHAIN: D, E;	(TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1503	1awc	B	880	1045	1.7e-29	0.05	-0.11		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1503	1bd8		697	862	3.4e-26	0.26	0.98		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1503	1bd8		776	937	4.5e-32	0.60	1.00		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1503	1blx	B	695	868	1.1e-26	0.37	0.99		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1503	1blx	B	697	862	1.4e-24	0.07	0.76		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1503	1blx	B	779	941	7.5e-33	0.64	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1503	1bu9	A	697	867	3.4e-31	0.42	0.84		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1503	1bu9	A	748	894	6.8e-32	0.39	0.99		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1503	1d9s	A	693	833	3e-19	0.23	0.77		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
1503	1d9s	A	776	909	1.2e-32	0.81	1.00		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
1503	1dcq	A	685	881	1.4e-21	-0.07	0.65		PYK2-ASSOCIATED PROTEIN BETA; CHAIN: A;	METAL BINDING PROTEIN ZINC-BINDING MODULE, ANKYRIN REPEATS, METAL BINDING PROTEIN
1503	1ihb	A	697	866	1.7e-30	0.22	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1503	1ihb	A	748	894	6.8e-32	0.52	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1503	1ikn	D	640	812	1.7e-31	0.21	0.31		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1503	1ikn	D	693	912	3e-34	0.10	1.00		B-ALPHA; CHAIN: D; NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B- ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1503	1ikn	D	722	882	3.4e-38	0.37	1.00		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B- ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1503	1ikn	D	747	947	3e-41	0.52	1.00		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B- ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1503	1ikn	D	776	983	3e-38	0.37	1.00		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B- ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1503	1nfi	E	640	812	1.7e-31	0.15	0.88		NF-KAPPA-B P65; CHAIN: A; C; NF-KAPPA-B P50; CHAIN: B; D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1503	1nfi	E	693	909	7.5e-34	0.43	1.00		NF-KAPPA-B P65; CHAIN: A; C; NF-KAPPA-B P50; CHAIN: B; D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1503	1nfi	E	721	882	8.5e-38	0.42	1.00		NF-KAPPA-B P65; CHAIN: A; C; NF-KAPPA-B P50; CHAIN: B; D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1503	1nfi	E	776	982	3e-35	0.50	1.00		NF-KAPPA-B P65; CHAIN: A; C; NF-KAPPA-B P50; CHAIN: B; D;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									I-KAPPA-B-ALPHA; CHAIN: E, F;	(TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1504	1a26		958	1128	1e-35	0.01	0.52		POLY (ADP-RIBOSE) POLYMERASE; CHAIN: NULL;	TRANSFERASE PARP-CF, POLY(ADP-RIBOSE) TRANSFERASE, POLY TRANSFERASE, GLYCOSYLTRANSFERASE, NAD(+) 2 ADP-RIBOSYLTRANSFERASE
1504	1a26		994	1127	1.7e-08	-0.24	0.16		POLY (ADP-RIBOSE) POLYMERASE; CHAIN: NULL;	TRANSFERASE PARP-CF, POLY(ADP-RIBOSE) TRANSFERASE, POLY TRANSFERASE, GLYCOSYLTRANSFERASE, NAD(+) 2 ADP-RIBOSYLTRANSFERASE
1504	1awc	B	128	296	3.4e-35	0.46	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1504	1awc	B	185	329	6.8e-39	0.22	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1504	1awc	B	215	357	1.7e-36	0.15	0.86		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1504	lawc	B	25	164	3e-43	0.62	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1504	lawc	B	26	176	1.5e-39	0.75	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1504	lawc	B	335	482	1.2e-33	0.69	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1504	lawc	B	402	578	1.2e-37	0.17	0.95		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1504	1awc	B	437	611	3.4e-33	0.04	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1504	1awc	B	491	644	4.5e-47	0.49	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1504	1awc	B	491	644	4.5e-47			105.28	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1504	1awc	B	496	640	8.5e-39	0.47	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1504	1awc	B	645	784	3e-42	0.64	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA I; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1504	1awc	B	660	797	3.4e-38	0.49	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA I; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1504	1awc	B	683	817	1.2e-35	0.28	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA I; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1504	1awc	B	89	296	1.4e-40	-0.00	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA I; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1504	1b0x	A	877	933	9e-07	1.27	1.00		EPHA4 RECEPTOR TYROSINE KINASE; CHAIN: A;	TRANSFERASE RECEPTOR TYROSINE KINASE, PROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										INTERACTION MODULE, 2 DIMERIZATION DOMAIN, TRANSFERASE
1504	1b0x	A	877	941	3.4e-06	1.08	1.00		EPHA4 RECEPTOR TYROSINE KINASE; CHAIN: A;	TRANSFERASE RECEPTOR TYROSINE KINASE, PROTEIN INTERACTION MODULE, 2 DIMERIZATION DOMAIN, TRANSFERASE
1504	1b4f	A	875	935	0.00014	0.82	0.99		EPHB2; CHAIN: A, B, C, D, E, F, G, H;	SIGNAL TRANSDUCTION SAM DOMAIN, EPH RECEPTOR, SIGNAL TRANSDUCTION, OLIGOMER
1504	1b4f	A	877	933	4.5e-10	0.72	0.99		EPHB2; CHAIN: A, B, C, D, E, F, G, H;	SIGNAL TRANSDUCTION SAM DOMAIN, EPH RECEPTOR, SIGNAL TRANSDUCTION, OLIGOMER
1504	1bd8		179	317	4.5e-36	0.43	1.00		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1504	1bd8		24	164	3e-39	0.67	1.00		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1504	1bd8		332	483	1e-28	0.67	1.00		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1504	1bd8		402	581	3e-34	0.13	0.98		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1504	1bd8		433	614	7.5e-39	0.14	1.00		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1504	1bd8		492	643	1.5e-42	0.82	1.00		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1504	1bd8		525	701	1.5e-41	0.09	1.00		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR,

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1504	1bd8		594	767	6e-41	0.31	1.00		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	ANKYRIN MOTIF TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1504	1bd8		62	266	4.5e-39	0.09	0.94		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1504	1bd8		644	784	3e-41	0.50	1.00		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1504	1bd8		660	800	1e-28	0.51	1.00		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1504	1bd8		683	818	1.4e-28	0.47	0.99		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1504	1bd8		95	299	1.2e-37	-0.32	0.53		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1504	1blx	B	179	317	1.5e-35	0.45	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1504	1blx	B	248	459	1.2e-31	-0.31	0.01		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1504	1blx	B	26	164	1.5e-39	0.60	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1504	1blx	B	332	483	4.5e-30	0.49	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR
1504	1blx	B	435	618	1.5e-41	0.34	0.99		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR
1504	1blx	B	494	643	7.5e-42	0.72	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR
1504	1blx	B	594	771	4.5e-45	0.17	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR
1504	1blx	B	648	784	9e-40	0.59	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR
1504	1blx	B	660	800	8.5e-28	0.54	1.00		CYCLIN-DEPENDENT KINASE	COMPLEX (INHIBITOR PROTEIN/KINASE)

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									6; CHAIN: A; P19INK4D; CHAIN: B;	PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1504	1blx	B	683	818	1.4e-28	0.30	0.99		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1504	1bu9	A	182	334	1.7e-36	0.28	0.92		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1504	1bu9	A	28	176	1.2e-35	0.85	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1504	1bu9	A	496	640	1.4e-32	0.64	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1504	1bu9	A	663	802	5.1e-33	0.57	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1504	1d9s	A	485	617	6e-35	0.63	1.00		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
1504	1d9s	A	49	164	3e-35	0.27	1.00		CYCLIN-DEPENDENT KINASE	SIGNALING PROTEIN HELIX-TURN-

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1504	1d9s	A	517	643	7.5e-38	0.32	1.00		4 INHIBITOR B; CHAIN: A; CYCLIN-DEPENDENT KINASE	HELIX, ANKYRIN REPEAT SIGNALING PROTEIN HELIX-TURN- HELIX, ANKYRIN REPEAT
1504	1d9s	A	585	770	6e-37	0.17	0.45		4 INHIBITOR B; CHAIN: A; CYCLIN-DEPENDENT KINASE	SIGNALING PROTEIN HELIX-TURN- HELIX, ANKYRIN REPEAT
1504	1ihb	A	182	333	8.5e-36	0.40	1.00		6 INHIBITOR; CHAIN: A, B; CYCLIN-DEPENDENT KINASE	CELL CYCLE INHIBITOR P18- INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1504	1ihb	A	28	176	1.2e-35	0.84	1.00		6 INHIBITOR; CHAIN: A, B; CYCLIN-DEPENDENT KINASE	CELL CYCLE INHIBITOR P18- INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1504	1ihb	A	496	640	1.4e-32	0.68	1.00		6 INHIBITOR; CHAIN: A, B; CYCLIN-DEPENDENT KINASE	CELL CYCLE INHIBITOR P18- INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1504	1ihb	A	663	801	1.7e-32	0.47	1.00		6 INHIBITOR; CHAIN: A, B; CYCLIN-DEPENDENT KINASE	CELL CYCLE INHIBITOR P18- INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1504	likn	D	156	366	1.2e-35	-0.18	0.00		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA- B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1504	likn	D	210	403	1.7e-33	-0.38	0.30		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA- B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1504	likn	D	28	240	1.5e-48	0.36	1.00		NF-KAPPA-B P65 SUBUNIT;	TRANSCRIPTION FACTOR P65;

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1504	likn	D	399	562	1.4e-30	-0.26	0.30		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1504	likn	D	525	715	5.1e-34	-0.26	0.06		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1504	likn	D	528	775	6e-60	-0.05	0.55		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1504	likn	D	558	748	1.7e-36	-0.36	0.25		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1504	likn	D	672	817	1.7e-36	0.20	0.92		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1504	likn	D	90	296	8.5e-40	-0.05	0.80		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1504	likn	D	91	396	4.5e-40	-0.19	0.12		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1504	lmyo		213	317	3e-35	0.09	0.98		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
1504	lmyo		365	482	6e-30	0.57	1.00		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN,

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1504	1myo		528	644	3e-39	0.51	1.00		MYOTROPHIN; CHAIN: NULL	ACETYLATION, NMR, ANK-REPEAT ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
1504	1myo		61	165	1.5e-38	0.03	1.00		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
1504	1myo		681	794	7.5e-39	0.66	1.00		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
1504	1myo		684	799	6.8e-25	0.57	0.86		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
1504	1nfi	E	154	366	6.8e-36	-0.11	0.58		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1504	1nfi	E	154	424	1.5e-40	-0.17	0.93		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1504	1nfi	E	208	458	1.2e-44	-0.34	0.36		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1504	1nfi	E	209	403	5.1e-33	-0.01	0.96		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1504	1nfi	E	365	622	1.5e-50	0.08	0.41		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1504	Infi	E	429	643	3e-45	0.08	0.95		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1504	Infi	E	463	628	5.1e-37	0.35	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1504	Infi	E	490	682	1.7e-32	0.34	0.99		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1504	Infi	E	528	777	6e-57	-0.06	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1504	Infi	E	61	307	1.3e-54	-0.13	0.49		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1504	Infi	E	672	817	1.7e-36	0.22	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1504	Infi	E	88	296	6.8e-40	0.12	0.98		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQPOL D score	Coumpound	PDB annotation
1504	1sgg		875	935	0.00034	0.65	0.84		EPHRIN TYPE-B RECEPTOR 2; CHAIN: NULL;	ANKYRIN 2 REPEAT HELIX TYROSINE-PROTEIN KINASE NMR, RECEPTOR OLIGOMERIZATION, EPH RECEPTORS, TYROSINE 2 PHOSPHORYLATION, SIGNAL TRANSDUCTION, TYROSINE- PROTEIN 3 KINASE
1504	1sgg		877	933	1.5e-09	0.78	0.59		EPHRIN TYPE-B RECEPTOR 2; CHAIN: NULL;	TYROSINE-PROTEIN KINASE NMR, RECEPTOR OLIGOMERIZATION, EPH RECEPTORS, TYROSINE 2 PHOSPHORYLATION, SIGNAL TRANSDUCTION, TYROSINE- PROTEIN 3 KINASE
1504	1sw6	A	527	784	6e-37	-0.22	0.18		REGULATORY PROTEIN SWI6; CHAIN: A, B;	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ANKYRIN REPEATS, CELL-CYCLE
1504	1yes	B	366	569	6e-30	-0.13	0.84		P53; CHAIN: A; 53BP2; CHAIN: B;	COMPLEX (ANTI- ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI- ONCOGENE/ANKYRIN REPEATS)
1504	1yes	B	528	722	4.5e-40	-0.03	1.00		P53; CHAIN: A; 53BP2; CHAIN: B;	COMPLEX (ANTI- ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI- ONCOGENE/ANKYRIN REPEATS)

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1504	1ycs	B	59	254	7.5e-39	0.01	0.76		P53; CHAIN: A; 53BP2; CHAIN: B;	COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS)
1507	1al7		39	190	1.7e-29	-0.10	0.05		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
1507	1bor		218	262	3e-14	-0.76	0.13		TRANSCRIPTION FACTOR PML; CHAIN: NULL;	TRANSCRIPTION REGULATION PROTO-ONCOGENE, NUCLEAR BODIES (PODS), LEUKEMIA, 2 TRANSCRIPTION REGULATION
1507	1chc		221	262	6e-14	-0.25	0.82		VIRUS EQUINE HERPES VIRUS-1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	
1507	1e96	B	40	191	3.4e-14	0.02	-0.03		RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	SIGNALING COMPLEX RAC1; P67PHOX; SIGNALLING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF
1507	1elr	A	39	161	6.8e-22	0.05	0.31		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1507	1elw	A	24	110	1.5e-11	0.00	-0.02		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN:	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									C, D;	REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1507	1elw	A	39	153	1.4e-21	0.13	0.24		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1507	1g25	A	221	262	4.5e-13	-0.20	0.37		CDK-ACTIVATING KINASE ASSEMBLY FACTOR MAT1; CHAIN: A;	METAL BINDING PROTEIN RING FINGER PROTEIN MAT1; RING FINGER (C3HC4)
1507	1rmd		210	302	9e-17	0.13	0.84		RAG1; CHAIN: NULL;	DNA-BINDING PROTEIN V(D)J RECOMBINATION ACTIVATING PROTEIN 1; RAG1, V(D)J RECOMBINATION, ANTIBODY, MAD, RING FINGER, 2 ZINC BINUCLEAR CLUSTER, ZINC FINGER, DNA-BINDING PROTEIN
1508	1adq	L	352	531	8.5e-18	-0.07	0.64		IGG4 REA; CHAIN: A; RF-AN IGM/LAMBDA; CHAIN: H, L;	COMPLEX (IMMUNOGLOBULIN/AUTOANTIGEN) COMPLEX (IMMUNOGLOBULIN/AUTOANTIGEN), RHEUMATOID FACTOR 2 AUTO-ANTIBODY COMPLEX
1508	1bih	A	262	628	5.1e-43	0.18	0.39		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1508	1bih	A	350	721	1.5e-43	0.34	0.49		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1508	1bih	A	449	812	1.7e-50	0.29	0.96		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1508	1bih	A	450	813	1.7e-50			124.44	HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1508	1bih	A	4	335	5.1e-37	0.00	-0.07		HEMOLIN; CHAIN: A, B;	HOMOPHILIC ADHESION
1508	1bih	A	726	1073	6.8e-40	0.15	0.36		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1508	1bih	A	74	447	4.5e-37	0.06	0.49		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1508	1bih	A	816	1184	3.4e-46	0.18	0.21		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1508	1cdy		557	723	1.5e-15	0.42	0.42		T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: NULL;	T-CELL SURFACE GLYCOPROTEIN IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, T-CELL, 2 MHC, LIPOPROTEIN, T-CELL SURFACE GLYCOPROTEIN
1508	1cs6	A	178	535	8.5e-49	-0.05	0.53		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1508	1cs6	A	262	628	1.5e-49	0.07	0.41		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1508	1cs6	A	348	721	5.1e-63	0.15	0.62		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1508	1cs6	A	3	347	1e-44	0.08	-0.01		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1508	1cs6	A	449	813	3.4e-55	0.26	0.84		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1508	1cs6	A	536	897	5.1e-49	0.24	0.70		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1508	1cs6	A	64	448	6.8e-37	0.05	-0.08		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1508	1cs6	A	74	448	7.5e-39	0.07	-0.02		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1508	1cs6	A	829	1185	8.5e-48	0.04	0.24		AXONIN-1; CHAIN: A;	ADHESION
1508	1cvs	C	1009	1184	1.7e-38	0.13	-0.01		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	CELL ADHESION NEURAL CELL ADHESION GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1508	1cvs	C	1096	1260	5.1e-21	0.08	-0.19		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1508	1cvs	C	178	346	6.8e-21	-0.16	0.30		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1508	1cvs	C	2	146	3.4e-17	0.23	-0.15		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1508	1cvs	C	361	535	5.1e-23	0.17	0.21		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1508	1cvs	C	450	628	8.5e-38	-0.05	0.54		FIBROBLAST GROWTH	GROWTH FACTOR/GROWTH FACTOR RECEPTOR

SEQ ID NO;	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1508	1cvs	C	61	260	5.1e-24	-0.10	0.27		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1508	1cvs	C	642	812	8.5e-36	-0.42	0.21		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1508	1cvs	C	737	896	1.7e-24	0.07	-0.05		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1508	1cvs	C	813	996	1.7e-37	0.05	-0.15		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1508	1cvs	D	1009	1184	5.1e-34	0.23	0.06		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1508	1cvs	D	178	346	1.2e-21	-0.19	0.82		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	FACTOR RECEPTOR GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1508	1cvs	D	271	447	1.7e-33	0.15	0.01		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1508	1cvs	D	2	146	6.8e-19	0.19	-0.05		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1508	1cvs	D	361	535	8.5e-25	0.19	0.25		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1508	1cvs	D	450	628	3.4e-35	-0.02	0.71		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1508	1cvs	D	61	260	1.2e-22	0.13	0.30		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									FACTOR RECEPTOR 1; CHAIN: C, D;	TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1508	1cvs	D	642	812	1.2e-36	-0.31	0.00		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1508	1cvs	D	737	896	1.7e-25	0.11	0.04		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1508	1cvs	D	813	996	3.4e-34	0.04	-0.11		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1508	1cvs	D	911	1082	3.4e-23	0.20	0.00		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1508	1dgi	R	602	810	6e-22	-0.35	0.03		POLIOVIRUS RECEPTOR; CHAIN: R; VP1; CHAIN: 1; VP2; CHAIN: 2; VP3; CHAIN: 3; VP4; CHAIN: 4;	VIRUS/VIRAL PROTEIN, RECEPTOR CD155, PVR, HUMAN POLIOVIRUS, ELECTRON MICROSCOPY, 2 POLIOVIRUS-RECEPTOR COMPLEX, VIRUS/VIRAL PROTEIN, RECEPTOR
1508	1dgi	R	641	889	1.3e-23	-0.09	0.16		POLIOVIRUS RECEPTOR; CHAIN: R; VP1; CHAIN: 1; VP2;	VIRUS/VIRAL PROTEIN, RECEPTOR CD155, PVR, HUMAN POLIOVIRUS,

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: 2; VP3; CHAIN: 3; VP4; CHAIN: 4;	ELECTRON MICROSCOPY, 2 POLIOVIRUS-RECEPTOR COMPLEX, VIRUS/VIRAL PROTEIN, RECEPTOR
1508	1dgi	R	902	1184	3.4e-18	-0.36	0.00		POLIOVIRUS RECEPTOR; CHAIN: R; VPI; CHAIN: 1; VP2; CHAIN: 2; VP3; CHAIN: 3; VP4; CHAIN: 4;	VIRUS/VIRAL PROTEIN, RECEPTOR CDI55, PVR, HUMAN POLIOVIRUS, ELECTRON MICROSCOPY, 2 POLIOVIRUS-RECEPTOR COMPLEX, VIRUS/VIRAL PROTEIN, RECEPTOR
1508	1epf	A	178	346	6.8e-17	0.02	0.30		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1508	1epf	A	266	433	5.1e-28	0.11	0.42		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1508	1epf	A	354	517	3.4e-17	0.09	0.22		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1508	1epf	A	452	645	3e-24	0.34	0.92		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1508	1epf	A	539	722	3.4e-25	0.23	0.07		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1508	1epf	A	644	798	1.7e-20	0.02	0.99		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1508	1epf	A	815	997	4.5e-22	0.16	0.01		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1508	1epf	A	818	982	6.8e-19	0.25	0.75		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1508	1ev2	E	271	447	1e-29	-0.16	0.24		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2;

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1508	1ev2	E	361	535	5.1e-22	0.10	0.04		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1508	1ev2	E	454	628	1e-33	-0.05	0.07		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1508	1ev2	E	825	996	1.7e-31	0.06	-0.11		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1508	1ev2	G	1009	1188	5.1e-35	0.10	0.01		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1508	1ev2	G	178	350	8.5e-21	0.02	0.43		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1508	1ev2	G	1	152	8.5e-18	0.01	-0.05		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1508	1ev2	G	271	451	1.2e-32	0.13	0.18		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1508	1ev2	G	361	538	6.8e-24	0.41	0.69		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1508	1ev2	G	454	628	6.8e-34	-0.02	0.06		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1508	1ev2	G	549	724	1.7e-23	0.23	0.53		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1508	1ev2	G	61	264	1.2e-21	0.12	0.17		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN:	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									E, F, G, H;	SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1508	1ev2	G	651	816	6.8e-34	-0.35	0.15		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1508	1ev2	G	737	900	3.4e-25	0.08	0.23		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1508	1ev2	G	74	259	1.5e-22	0.18	0.51		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1508	1ev2	G	825	1000	1.7e-33	0.04	-0.15		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1508	1ev2	G	911	1087	6.8e-22	0.02	-0.01		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1508	1evt	C	178	346	5.1e-21	-0.26	0.33		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF1; FGFR1;

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE 1-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1508	1evt	C	271	447	8.5e-32	0.01	-0.06		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR1; FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE 1-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1508	1evt	C	2	146	3.4e-19	0.23	-0.09		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR1; FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE 1-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1508	1evt	C	450	628	3.4e-33	-0.15	0.18		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR1; FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE 1-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1508	1evt	C	552	703	3e-16	-0.01	0.19		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR1; FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE 1-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1508	1evt	C	61	260	1.2e-22	0.16	0.04		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR1; FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE 1-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1508	1evt	C	642	812	1.4e-35	-0.32	0.11		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR1; FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1508	1evt	C	737	896	1.2e-24	0.05	-0.03		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR1; FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1508	1f2q	A	349	538	1.5e-17	0.14	0.06		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A;	IMMUNE SYSTEM FC-EPSILON RI-ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN
1508	1f2q	A	39	153	3e-21	0.32	0.48		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A;	IMMUNE SYSTEM FC-EPSILON RI-ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN
1508	1f2q	A	415	539	1.5e-20	0.26	0.92		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A;	IMMUNE SYSTEM FC-EPSILON RI-ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN
1508	1f2q	A	605	727	9e-18	-0.01	0.63		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A;	IMMUNE SYSTEM FC-EPSILON RI-ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN
1508	1f2q	A	646	795	1.7e-21	0.05	0.17		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A;	IMMUNE SYSTEM FC-EPSILON RI-ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN
1508	1f2q	A	779	900	3e-19	0.04	0.12		HIGH AFFINITY IMMUNOGLOBULIN EPSILON	IMMUNE SYSTEM FC-EPSILON RI-ALPHA; IMMUNOGLOBULIN FOLD,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									RECEPTOR CHAIN: A;	GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN
1508	1f6a	A	258	430	3.4e-19	-0.01	0.01		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IG EPSILON CHAIN C REGION; CHAIN: B, D;	IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON) IGE-FC; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC
1508	1f6a	A	346	538	3.4e-17	0.09	-0.02		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IG EPSILON CHAIN C REGION; CHAIN: B, D;	IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON) IGE-FC; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC
1508	1f6a	A	39	152	6e-21	0.16	0.30		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IG EPSILON CHAIN C REGION; CHAIN: B, D;	IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON) IGE-FC; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC
1508	1f6a	A	415	538	9e-20	0.35	0.24		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IG EPSILON CHAIN C REGION; CHAIN: B, D;	IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON) IGE-FC; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC
1508	1f6a	A	451	645	7.5e-19	0.21	0.70		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IG EPSILON CHAIN C REGION; CHAIN: B, D;	IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON) IGE-FC; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC
1508	1f6a	A	566	726	7.5e-19	0.37	0.95		HIGH AFFINITY IMMUNOGLOBULIN EPSILON	IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON)

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Coumpound	PDB annotation
									RECEPTOR CHAIN: A; IG EPSILON CHAIN C REGION; CHAIN: B, D;	IGE-FC; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC
1508	1f6a	A	5	152	1e-16	0.20	-0.11		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IG EPSILON CHAIN C REGION; CHAIN: B, D;	IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON) IGE-FC; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC
1508	1f6a	A	646	795	1.4e-20	-0.14	0.11		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IG EPSILON CHAIN C REGION; CHAIN: B, D;	IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON) IGE-FC; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC
1508	1f6a	A	740	900	1.5e-19	0.27	0.10		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IG EPSILON CHAIN C REGION; CHAIN: B, D;	IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON) IGE-FC; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC
1508	1f6a	A	821	999	1.5e-15	0.11	0.65		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IG EPSILON CHAIN C REGION; CHAIN: B, D;	IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON) IGE-FC; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC
1508	1f6g	A	349	534	1.2e-17	0.38	0.55		FC RECEPTOR FC(GAMMA)RIIA; CHAIN: A;	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32; FC RECEPTOR, IMMUNOGLOBULIN, LEUKOCYTE, CD32
1508	1f6g	A	37	148	3e-19	0.28	0.86		FC RECEPTOR FC(GAMMA)RIIA; CHAIN: A;	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32; FC RECEPTOR,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										IMMUNOGLOBULIN, LEUKOCYTE, CD32
1508	1feg	A	456	645	6e-19	0.02	0.43		FC RECEPTOR FC(GAMMA)RIIA; CHAIN: A;	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32; FC RECEPTOR, IMMUNOGLOBULIN, LEUKOCYTE, CD32
1508	1feg	A	820	997	6.8e-17	-0.26	0.53		FC RECEPTOR FC(GAMMA)RIIA; CHAIN: A;	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32; FC RECEPTOR, IMMUNOGLOBULIN, LEUKOCYTE, CD32
1508	1fhg	A	1085	1186	8.5e-16	0.20	0.03		TELOKIN; CHAIN: A	CONTRACTILE PROTEIN IMMUNOGLOBULIN FOLD, BETA BARREL
1508	1fhg	A	347	447	8.5e-17	-0.28	0.00		TELOKIN; CHAIN: A	CONTRACTILE PROTEIN IMMUNOGLOBULIN FOLD, BETA BARREL
1508	1fml	A	36	148	3e-18	0.29	0.54		LOW AFFINITY IMMUNOGLOBULIN GAMMA FC REGION CHAIN: A;	IMMUNE SYSTEM RECEPTOR BETA SANDWICH, IMMUNOGLOBULIN-LIKE, RECEPTOR
1508	1fml	A	646	796	3.4e-16	0.03	0.41		LOW AFFINITY IMMUNOGLOBULIN GAMMA FC REGION CHAIN: A;	IMMUNE SYSTEM RECEPTOR BETA SANDWICH, IMMUNOGLOBULIN-LIKE, RECEPTOR
1508	1ge1	L	352	518	1.7e-15	0.17	0.60		ENVELOPE PROTEIN GP120; CHAIN: G; CD4; CHAIN: C; ANTIBODY 17B; CHAIN: L, H;	COMPLEX (HIV ENVELOPE PROTEIN/CD4/FAB) COMPLEX (HIV ENVELOPE PROTEIN/CD4/FAB), HIV-1 EXTERIOR 2 ENVELOPE GP120, T-CELL SURFACE
1508	1hng	A	557	703	6e-19	-0.34	0.06		T LYMPHOCYTE ADHESION GLYCOPROTEIN CD2 (RAT) 1HNG 3	GLYCOPROTEIN CD4, 3 ANTIGEN-BINDING FRAGMENT OF HUMAN IMMUNOGLOBULIN 17B, 4 GLYCOSYLATED PROTEIN

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1508	1hng	A	825	996	9e-15	0.06	0.17		T LYMPHOCYTE ADHESION GLYCOPROTEIN CD2 (RAT) 1HNG 3	
1508	1itb	B	462	679	1.5e-20	-0.02	0.18		INTERLEUKIN-1 BETA; CHAIN: A; TYPE 1 INTERLEUKIN-1 RECEPTOR; CHAIN: B;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR)
1508	1itb	B	740	996	3e-20	0.42	0.09		INTERLEUKIN-1 BETA; CHAIN: A; TYPE 1 INTERLEUKIN-1 RECEPTOR; CHAIN: B;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR)
1508	1itb	B	747	994	1.7e-15	0.10	0.55		INTERLEUKIN-1 BETA; CHAIN: A; TYPE 1 INTERLEUKIN-1 RECEPTOR; CHAIN: B;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR)
1508	1koa		1084	1185	3.4e-14	0.14	0.59		TWITCHIN; CHAIN: NULL;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
1508	1lil	A	355	531	8.5e-16	0.20	0.60		LAMBDA III BENCE JONES PROTEIN CLE; CHAIN: A, B	IMMUNOGLOBULIN IMMUNOGLOBULIN, BENCE JONES PROTEIN
1508	1mco	H	143	543	5.1e-17			104.67	IMMUNOGLOBULIN IMMUNOGLOBULIN G1 (IGG1) (MCG) WITH A HINGE DELETION IMCO 3	
1508	1mco	H	538	884	1.5e-17	-0.05	0.23		IMMUNOGLOBULIN	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1508	Inct		1086	1185	1.7e-14	0.58	0.53		IMMUNOGLOBULIN G1 (JGG1) (MCG) WITH A HINGE DELETION IMCO 3 TITIN; CHAIN: NULL;	MUSCLE PROTEIN CONNECTIN, NEXTM5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN
1508	Inct		178	262	3.4e-11	-0.53	0.00		TITIN; CHAIN: NULL;	MUSCLE PROTEIN CONNECTIN, NEXTM5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN
1508	Inct		349	449	5.1e-15	0.16	-0.12		TITIN; CHAIN: NULL;	MUSCLE PROTEIN CONNECTIN, NEXTM5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN
1508	Inct		643	721	1.7e-13	0.46	0.04		TITIN; CHAIN: NULL;	MUSCLE PROTEIN CONNECTIN, NEXTM5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN
1508	Inkr		26	149	3.4e-10	0.11	-0.07		P58-CL42 KIR; CHAIN: NULL;	INHIBITORY RECEPTOR KILLER CELL INHIBITORY RECEPTOR; INHIBITORY RECEPTOR, NATURAL

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1508	1nkr		813	995	1.7e-23	-0.01	0.13		P58-CL42 KIR; CHAIN: NULL;	KILLER CELLS, IMMUNOLOGICAL 2 RECEPTORS, IMMUNOGLOBULIN FOLD
1508	1tnm		1088	1185	1.7e-14	0.63	0.35		MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) 1TNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) 1TNM 4 1TNM 58	INHIBITORY RECEPTOR KILLER CELL INHIBITORY RECEPTOR; INHIBITORY RECEPTOR, NATURAL KILLER CELLS, IMMUNOLOGICAL 2 RECEPTORS, IMMUNOGLOBULIN FOLD
1508	1tnm		178	262	3.4e-11	-0.22	0.00		MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) 1TNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) 1TNM 4 1TNM 58	
1508	1tnm		2	61	1.5e-09	0.30	-0.15		MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) 1TNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) 1TNM 4 1TNM 58	
1508	1tnm		643	721	1.7e-13	0.50	0.04		MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) 1TNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) 1TNM 4 1TNM 58	
1508	1vca	A	397	538	4.5e-15	-0.05	0.72		HUMAN VASCULAR CELL ADHESION MOLECULE-1; 1VCA 4 CHAIN: A, B; 1VCA 5	CELL ADHESION PROTEIN VCAM-D1,2; 1VCA 6 IMMUNOGLOBULIN SUPERFAMILY, INTEGRIN-BINDING 1VCA 15
1508	1vca	A	557	680	4.5e-13	-0.15	0.00		HUMAN VASCULAR CELL	CELL ADHESION PROTEIN VCAM-

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1508	1wio	A	364	703	1.2e-26	0.09	0.41		ADHESION MOLECULE-1; IVCA 4 CHAIN: A, B; IVCA 5	D1.2; IVCA 6 IMMUNOGLOBULIN SUPERFAMILY, INTEGRIN-BINDING IVCA 15
1508	1wio	A	552	882	6e-26	-0.11	0.13		T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: A, B;	GLYCOPROTEIN CD4; IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, T-CELL, 2 MHC LIPOPROTEIN, POLYMORPHISM
1508	1wio	A	740	1068	6e-23	0.06	0.68		T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: A, B;	GLYCOPROTEIN CD4; IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, T-CELL, 2 MHC LIPOPROTEIN, POLYMORPHISM
1508	1zxq		821	1000	1.5e-16	-0.09	0.05		INTERCELLULAR ADHESION MOLECULE-2; CHAIN: NULL;	CELL ADHESION ICAM-2; IMMUNOGLOBULIN FOLD, CELL ADHESION, GLYCOPROTEIN, 2 TRANSMEMBRANE, REPEAT, SIGNAL
1508	2dli	A	347	534	1.2e-19	0.19	-0.09		MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	IMMUNE SYSTEM P38 NATURAL KILLER CELL RECEPTOR; KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN
1508	2dli	A	451	643	4.5e-24	0.28	0.05		MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	IMMUNE SYSTEM P38 NATURAL KILLER CELL RECEPTOR; KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN
1508	2dli	A	536	723	3e-16	0.00	0.19		MHC CLASS I NK CELL	IMMUNE SYSTEM P38 NATURAL

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									RECEPTOR PRECURSOR; CHAIN: A;	KILLER CELL RECEPTOR; KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN
1508	2dli	A	67	256	3e-21	0.20	0.23		MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	IMMUNE SYSTEM P58 NATURAL KILLER CELL RECEPTOR; KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN
1508	2dli	A	7	148	1.2e-09	0.22	-0.06		MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	IMMUNE SYSTEM P58 NATURAL KILLER CELL RECEPTOR; KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN
1508	2dli	A	813	991	5.1e-22	0.17	-0.06		MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	IMMUNE SYSTEM P58 NATURAL KILLER CELL RECEPTOR; KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN
1508	2feb	A	152	349	7.5e-15	0.01	-0.02		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
1508	2feb	A	349	537	3.4e-18	0.25	0.27		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
1508	2feb	A	37	151	7.5e-21	0.28	0.75		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
1508	2feb	A	415	536	3e-20	-0.04	0.65		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
1508	2feb	A	528	724	1.2e-16	0.19	0.65		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
1508	2feb	A	740	898	3e-20	0.38	0.47		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
1508	2feb	A	820	999	3.4e-17	0.04	0.00		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
1508	2feb	A	825	998	4.5e-19	0.08	-0.05		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1508	2feb	A	917	1086	3e-18	0.00	0.70		FC GAMMA RIIB; CHAIN: A;	FC, CD32, IMMUNE SYSTEM
1508	3ncm	A	642	722	1.7e-12	0.42	0.12		NEURAL CELL ADHESION MOLECULE, LARGE ISOFORM; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
1508	8fab	A	353	529	5.1e-18	0.05	0.47		IMMUNOGLOBULIN FAB FRAGMENT FROM HUMAN IMMUNOGLOBULIN IGG1 (LAMBDA, HIL) 8FAB 3	CELL ADHESION PROTEIN NCAM MODULE 2; CELL ADHESION, GLYCOPROTEIN, HEPARIN-BINDING, GPI-ANCHOR, 2 NEURAL ADHESION MOLECULE, IMMUNOGLOBULIN FOLD, HOMOPHILIC 3 BINDING, CELL ADHESION PROTEIN
1510	1c7j	A	4	64	9e-13	-0.24	0.22		PARA-NITROBENZYL ESTERASE; CHAIN: A;	HYDROLASE PNB ESTERASE; ALPHA-BETA HYDROLASE, DIRECTED EVOLUTION, ORGANIC ACTIVITY, 2 PNB ESTERASE
1510	1ea5	A	3	73	1e-21	-0.23	0.12		ACETYLCHOLINESTERASE; CHAIN: A;	CHOLINESTERASE SERINE HYDROLASE, NEUROTRANSMITTER CLEAVAGE, CATALYTIC 2 TRIAD, ALPHA/BETA HYDROLASE
1510	1maa	A	3	73	5.1e-22	-0.29	0.43		ACETYLCHOLINESTERASE; CHAIN: A, B, C, D;	HYDROLASE MACHE; HYDROLASE, SERINE ESTERASE, ACETYLCHOLINESTERASE, TETRAMER, 2 HYDROLASE FOLD, GLYCOSYLATED PROTEIN
1510	2bce		3	74	3.4e-19	-0.50	0.06		CHOLESTEROL ESTERASE; CHAIN: NULL;	HYDROLASE BILE SALT ACTIVATED LIPASE, BILE SALT STIMULATED HYDROLASE, SERINE ESTERASE, LIPASE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1512	1mey	G	241	274	3.4e-08	0.14	-0.11		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1512	2adr		1	39	5.1e-11	-0.78	0.03		ADRI; CHAIN: NULL;	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ADRI, ZINC FINGER, NMR
1512	2adr		403	446	1.7e-11	0.09	-0.20		ADRI; CHAIN: NULL;	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ADRI, ZINC FINGER, NMR
1514	2pro	A	81	166	4.5e-10	0.03	-0.19		ALPHA-LYTIC PROTEASE; CHAIN: A, B, C;	PRO REGION PRO REGION, FOLDASE, PROTEIN FOLDING, SERINE PROTEASE
1515	1ez3	A	432	543	4.5e-09	-0.01	0.09		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
1521	1a4y	A	164	500	5.1e-25	0.21	1.00		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPI TOPE MAPPING, LEUCINE-RICH 3 REPEATS
1521	1a4y	A	243	469	3e-34	0.34	1.00		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPI TOPE MAPPING, LEUCINE-RICH 3 REPEATS

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1521	1a4y	A	282	469	3e-35	0.51	1.00		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS
1521	1a4y	A	2	407	3.4e-24	0.05	0.95		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS
1521	1a4y	A	2	496	6.8e-32			113.01	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS
1521	1a4y	A	86	471	6.8e-32	-0.03	0.90		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS
1521	1d0b	A	267	438	1.2e-23	-0.27	0.48		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1521	1d0b	A	316	495	1.7e-21	-0.30	0.39		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1521	1dce	A	350	474	1.7e-10	0.07	0.19		RAB GERANYLGERANYLTRANSFE RASE ALPHA SUBUNIT; CHAIN: A, C; RAB	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1521	1fo1	A	401	471	1.5e-06	-0.04	0.39		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1521	1fo1	B	401	471	1.5e-06	-0.07	0.28		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1521	1fqv	A	254	512	1.7e-12	-0.00	0.03		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1521	1fs2	A	323	514	8.5e-13	0.08	0.51		SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	LIGASE CYCLIN A/CDK2-ASSOCIATED P45; CYCLIN A/CDK2-ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
1521	1yrg	A	157	418	6.8e-19	-0.08	0.55		GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	TRANSCRIPTION RNA1P; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPII, GTPASE-ACTIVATING PROTEIN, GAP, RNA1P, RANGAP, LRR, LEUCINE- 2 RICH REPEAT PROTEIN, TWINNING, HEMIREDIAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
1521	1yrg	A	215	474	5.1e-21	0.17	0.98		GTPASE-ACTIVATING PROTEIN RNA1_SCHPO;	TRANSCRIPTION RNA1P; RANGAP; GTPASE-ACTIVATING PROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									CHAIN: A, B;	FOR SPI1, GTPASE-ACTIVATING PROTEIN, GAP, RNAIP, RANGAP, LRR, LEUCINE- 2 RICH REPEAT PROTEIN, TWINNING, HEMIREDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
1521	1yrq	A	243	469	4.5e-30	0.11	0.55		GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	TRANSCRIPTION RNAIP; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPI1, GTPASE-ACTIVATING PROTEIN, GAP, RNAIP, RANGAP, LRR, LEUCINE- 2 RICH REPEAT PROTEIN, TWINNING, HEMIREDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
1521	1yrq	A	348	508	3.4e-09	0.10	0.28		GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	TRANSCRIPTION RNAIP; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPI1, GTPASE-ACTIVATING PROTEIN, GAP, RNAIP, RANGAP, LRR, LEUCINE- 2 RICH REPEAT PROTEIN, TWINNING, HEMIREDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
1521	2bnh		42	491	8.5e-46			109.97	RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1521	2bnh		89	511	8.5e-46	0.12	0.81		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1522	1c1g	A	54	142	4.5e-08	0.46	-0.20		TROPOMYOSIN; CHAIN: A, B, C, D	CONTRACTILE PROTEIN TROPOMYOSIN COILED-COIL ALPHA-HELICAL, CONTRACTILE PROTEIN
1522	1c1i		50	142	1.5e-08	0.36	-0.20		COLICIN 1A; CHAIN: NULL;	TRANSMEMBRANE PROTEIN COLICIN, BACTERIOCIN, ION CHANNEL FORMATION, TRANSMEMBRANE 2 PROTEIN
1522	1ez3	A	50	143	1.1e-12	0.36	-0.14		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
1522	1req	A	50	142	4.5e-08	0.11	-0.20		METHYLMALONYL-COA MUTASE; CHAIN: A, B, C, D;	ISOMERASE ISOMERASE, MUTASE, INTRAMOLECULAR TRANSFERASE
1523	1fqv	B	17	82	1.7e-24	0.78	1.00		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1523	1fs1	B	17	82	1.7e-24	0.21	0.62		CYCLIN A/CDK2-ASSOCIATED P19; CHAIN: A, C; CYCLIN A/CDK2-ASSOCIATED P45; CHAIN: B, D;	LIGASE SKP2 F-BOX; SKP1; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1523	1fs2	B	17	82	1.7e-24	0.48	0.99		SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	LIGASE CYCLIN A/CDK2-ASSOCIATED P45; CYCLIN A/CDK2-ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
1523	1veb	B	17	80	3.4e-16	0.76	1.00		ELONGIN B; CHAIN: A, D, G, J; ELONGIN C; CHAIN: B, E, H, K; VHL; CHAIN: C, F, I, L;	TRANSCRIPTION TUMOR SUPPRESSOR, CANCER, UBIQUITIN, BETA SANDWICH, 2

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										TRANSCRIPTION, TRANSCRIPTIONAL ELONGATION
1523	1vcb	B	17	84	3.4e-16			52.02	ELONGIN B; CHAIN: A, D, G, J; ELONGIN C; CHAIN: B, E, H, K; VHL; CHAIN: C, F, I, L;	TRANSCRIPTION TUMOR SUPPRESSOR, CANCER, UBIQUITIN, BETA SANDWICH, 2 TRANSCRIPTION, TRANSCRIPTIONAL ELONGATION
1524	1pbw	A	122	291	6.8e-19	0.10	0.63		PHOSPHATIDYLINOSITOL 3-KINASE; CHAIN: A, B;	PHOSPHOTRANSFERASE RHOGAP DOMAIN; PHOSPHOTRANSFERASE, TPASE ACTIVATING PROTEIN, GAP, CDC42, 2 PHOSPHOINOSITIDE 3-KINASE, SH3 DOMAIN, SH2 DOMAIN, 3 SIGNAL TRANSDUCTION
1524	1pbw	A	125	304	4.5e-35	0.57	1.00		PHOSPHATIDYLINOSITOL 3-KINASE; CHAIN: A, B;	PHOSPHOTRANSFERASE RHOGAP DOMAIN; PHOSPHOTRANSFERASE, TPASE ACTIVATING PROTEIN, GAP, CDC42, 2 PHOSPHOINOSITIDE 3-KINASE, SH3 DOMAIN, SH2 DOMAIN, 3 SIGNAL TRANSDUCTION
1524	1pbw	B	107	312	3e-36			67.87	PHOSPHATIDYLINOSITOL 3-KINASE; CHAIN: A, B;	PHOSPHOTRANSFERASE RHOGAP DOMAIN; PHOSPHOTRANSFERASE, TPASE ACTIVATING PROTEIN, GAP, CDC42, 2 PHOSPHOINOSITIDE 3-KINASE, SH3 DOMAIN, SH2 DOMAIN, 3 SIGNAL TRANSDUCTION
1524	1pbw	B	122	291	6.8e-19	0.09	0.76		PHOSPHATIDYLINOSITOL 3-KINASE; CHAIN: A, B;	PHOSPHOTRANSFERASE RHOGAP DOMAIN; PHOSPHOTRANSFERASE, TPASE ACTIVATING PROTEIN, GAP, CDC42, 2 PHOSPHOINOSITIDE 3-KINASE, SH3 DOMAIN, SH2

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										DOMAIN, 3 SIGNAL TRANSDUCTION
1524	1pbw	B	125	311	3e-36	0.44	0.95		PHOSPHATIDYLINOSITOL 3-KINASE; CHAIN: A, B;	PHOSPHOTRANSFERASE RHOGAP DOMAIN; PHOSPHOTRANSFERASE, TPASE ACTIVATING PROTEIN, GAP, CDC42, 2 PHOSPHOINOSITIDE 3-KINASE, SH3 DOMAIN, SH2 DOMAIN, 3 SIGNAL TRANSDUCTION
1524	1rgp		112	308	1.5e-37	0.77	1.00		RHOGAP; CHAIN: NULL;	G-PROTEIN CDC42 GTPASE-ACTIVATING PROTEIN; G-PROTEIN, GAP, SIGNAL-TRANSDUCTION
1524	1rgp		88	277	1e-29	0.08	0.54		RHOGAP; CHAIN: NULL;	G-PROTEIN CDC42 GTPASE-ACTIVATING PROTEIN; G-PROTEIN, GAP, SIGNAL-TRANSDUCTION
1524	1rgp		88	308	1.5e-37			97.96	RHOGAP; CHAIN: NULL;	G-PROTEIN CDC42 GTPASE-ACTIVATING PROTEIN; G-PROTEIN, GAP, SIGNAL-TRANSDUCTION
1524	1tx4	A	112	308	7.5e-39	0.88	1.00		P50-RHOGAP; CHAIN: A; TRANSFORMING PROTEIN RHOA; CHAIN: B;	COMPLEX(GTPASE ACTIVATN/PROTO-ONCOGENE) GTPASE-ACTIVATING PROTEIN RHOGAP; COMPLEX (GTPASE ACTIVATION/PROTO-ONCOGENE), GTPASE, 2 TRANSITION STATE, GAP
1524	1tx4	A	91	304	1.7e-29	0.18	1.00		P50-RHOGAP; CHAIN: A; TRANSFORMING PROTEIN RHOA; CHAIN: B;	COMPLEX(GTPASE ACTIVATN/PROTO-ONCOGENE) GTPASE-ACTIVATING PROTEIN RHOGAP; COMPLEX (GTPASE ACTIVATION/PROTO-ONCOGENE), GTPASE, 2 TRANSITION STATE, GAP
1524	1tx4	A	91	308	7.5e-39			107.06	P50-RHOGAP; CHAIN: A; TRANSFORMING PROTEIN RHOA; CHAIN: B;	COMPLEX(GTPASE ACTIVATN/PROTO-ONCOGENE) GTPASE-ACTIVATING PROTEIN RHOGAP; COMPLEX (GTPASE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										ACTIVATION/PROTO-ONCOGENE), GTPASE, 2 TRANSITION STATE, GAP
1525	layz	A	1	134	1e-40			92.22	UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN CONJUGATION UBC2; UBIQUITIN CONJUGATION, UBIQUITIN-CONJUGATING ENZYME
1525	layz	A	4	128	1e-40	0.61	1.00		UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN CONJUGATION UBC2; UBIQUITIN CONJUGATION, UBIQUITIN-CONJUGATING ENZYME
1525	lc4z	D	5	129	8.5e-33	0.36	0.99		UBIQUITIN-PROTEIN LIGASE E3A; CHAIN: A, B, C; UBIQUITIN CONJUGATING ENZYME E2; CHAIN: D;	LIGASE E6AP; UBCH7; BILOBAL STRUCTURE, ELONGATED SHAPE, E3 UBIQUITIN LIGASE, E2 2 UBIQUITIN CONJUGATING ENZYME
1525	lc4z	D	5	129	8.5e-33			80.53	UBIQUITIN-PROTEIN LIGASE E3A; CHAIN: A, B, C; UBIQUITIN CONJUGATING ENZYME E2; CHAIN: D;	LIGASE E6AP; UBCH7; BILOBAL STRUCTURE, ELONGATED SHAPE, E3 UBIQUITIN LIGASE, E2 2 UBIQUITIN CONJUGATING ENZYME
1525	lqcq	A	1	130	3.4e-51	0.57	1.00		UBIQUITIN CONJUGATING ENZYME; CHAIN: A;	LIGASE UBIQUITIN, UBIQUITIN-CONJUGATING ENZYME, YEAST
1525	lqcq	A	4	131	3.4e-51			106.20	UBIQUITIN CONJUGATING ENZYME; CHAIN: A;	LIGASE UBIQUITIN, UBIQUITIN-CONJUGATING ENZYME, YEAST
1525	lu9a	A	1	130	3.4e-38	0.83	1.00		UBC9; CHAIN: NULL;	UBIQUITIN-CONJUGATING ENZYME UBIQUITIN-CONJUGATING ENZYME; UBIQUITIN-CONJUGATING ENZYME, UBIQUITIN-DIRECTED 2 PROTEOLYSIS, CELL CYCLE CONTROL, LIGASE
1525	lu9a	A	1	131	3.4e-38			73.11	UBC9; CHAIN: NULL;	UBIQUITIN-CONJUGATING ENZYME UBIQUITIN-CONJUGATING ENZYME; UBIQUITIN-CONJUGATING ENZYME

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										ENZYME, UBIQUITIN-DIRECTED 2 PROTEOLYSIS, CELL CYCLE CONTROL, LIGASE
1525	2aak		1	126	1.2e-41			96.00	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION UBC1; UBIQUITIN CONJUGATION, LIGASE
1525	2aak		1	127	1.2e-41	0.49	1.00		UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION UBC1; UBIQUITIN CONJUGATION, LIGASE
1525	2e2c		1	132	1.5e-37			82.57	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION UBIQUITIN CONJUGATION, UBIQUITIN CARRIER PROTEIN, THIOESTER 2 BOND, LIGASE
1525	2e2c		3	124	1.5e-37	0.66	1.00		UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION UBIQUITIN CONJUGATION, UBIQUITIN CARRIER PROTEIN, THIOESTER 2 BOND, LIGASE
1525	2ucz		2	132	1.7e-36			77.96	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION UBC7; UBIQUITIN CONJUGATION, LIGASE, YEAST
1525	2ucz		3	128	1.7e-36	0.80	1.00		UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION UBC7; UBIQUITIN CONJUGATION, LIGASE, YEAST
1527	1a4y	A	10	338	5.1e-19	-0.14	0.03		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS
1527	1a4y	A	10	473	3.4e-18			67.17	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1527	1a4y	A	134	335	9e-28	0.07	0.68		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS
1527	1a4y	A	25	415	3.4e-18	0.27	0.76		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS
1527	1a4y	A	66	309	1.5e-34	0.36	0.99		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS
1527	1a9n	A	140	284	3e-25	0.50	0.60		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1527	1a9n	A	164	291	7.5e-24	0.25	0.01		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1527	1a9n	A	212	326	1.5e-14	0.36	0.22		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1527	1a9n	A	232	339	3.4e-07	0.18	0.13		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1527	1a9n	A	43	146	1.7e-07	0.42	0.68		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1527	1a9n	A	51	187	1.5e-24	0.15	0.98		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1527	1a9n	A	92	234	3e-26	0.23	0.43		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1527	1a9n	C	140	290	4.5e-26	0.25	0.45		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1527	1a9n	C	212	326	9e-15	0.37	0.27		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1527	1a9n	C	23	95	3.4e-05	0.03	0.00		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1527	1a9n	C	43	146	1.7e-07	0.36	0.43		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1527	1a9n	C	51	187	3e-24	0.37	0.96		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1527	1a9n	C	68	215	1e-24	0.16	0.70		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B";	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: B, D;	(NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1527	1a9n	C	92	234	3e-26	0.43	0.69		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1527	1d0b	A	129	311	8.5e-24	0.35	0.99		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1527	1d0b	A	228	377	3.4e-18	-0.07	0.10		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1527	1d0b	A	4	188	3.4e-23	0.12	0.70		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1527	1dce	A	21	121	1.2e-10	0.31	0.15		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1527	1ds9	A	167	291	1.5e-18	-0.40	0.06		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1527	1ds9	A	217	338	5.1e-15	0.12	-0.09		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1527	1ds9	A	43	145	1e-09	-0.08	0.23		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1527	1ds9	A	73	235	1.4e-11	-0.39	0.15		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1527	1fo1	A	227	308	3.4e-07	-0.15	0.01		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1527	1fo1	B	227	308	3.4e-07	0.16	0.30		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1527	1fgv	A	134	347	1.5e-15	-0.05	0.36		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1527	1fs2	A	125	334	1.3e-20	0.21	-0.03		SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	LIGASE CYCLIN A/CDK2-ASSOCIATED P45; CYCLIN A/CDK2-ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
1527	1fs2	A	171	311	5.1e-12	0.00	0.04		SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	LIGASE CYCLIN A/CDK2-ASSOCIATED P45; CYCLIN A/CDK2-ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
1527	1yrg	A	62	360	6.8e-12	0.16	-0.03		GTPASE-ACTIVATING PROTEIN RNAI_SCHPO; CHAIN: A, B;	TRANSCRIPTION RNAIP; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPI1, GTPASE-ACTIVATING PROTEIN, GAP, RNAIP, RANGAP,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
										LRR, LEUCINE- 2 RICH REPEAT PROTEIN, TWINNING, 3 HEMIREDIAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
1527	lytg	A	86	265	1e-30	0.11	0.15		GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	TRANSCRIPTION RNA IP; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SP11, GTPASE-ACTIVATING PROTEIN, GAP, RNAIP, RANGAP, LRR, LEUCINE- 2 RICH REPEAT PROTEIN, TWINNING, 3 HEMIREDIAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
1527	2bnh		25	413	1.2e-22	0.08	0.74		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1527	2bnh		64	312	1.2e-40	0.01	0.81		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1528	la68		117	207	1.5e-13	0.66	0.86		POTASSIUM CHANNEL KV1.1; CHAIN: NULL;	POTASSIUM CHANNELS, POTASSIUM CHANNELS, TETRAMERIZATION DOMAIN, X-RAY 2 STRUCTURE, APLYSIA KV1.1
1528	ldsx	A	117	204	7.5e-12	0.09	0.28		KV1.2 VOLTAGE-GATED POTASSIUM CHANNEL; CHAIN: A, B, C, D, E, F, G, H;	SIGNALING PROTEIN VOLTAGE-GATED POTASSIUM CHANNEL, ASSEMBLY DOMAIN, TETRAMER
1528	lexb	E	117	210	1.2e-11	0.48	0.41		KV BETA2 PROTEIN; CHAIN: A; POTASSIUM CHANNEL KV1.1; CHAIN: E;	METAL TRANSPORT ION CHANNEL, OXIDOREDUCTASE, BETA SUBUNIT
1528	lqdv	A	117	208	3e-12	0.48	0.43		KV1.2 VOLTAGE-GATED	SIGNALING PROTEIN VOLTAGE-

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									POTASSIUM CHANNEL; CHAIN: A, B, C, D;	GATED POTASSIUM CHANNEL, TETRAMERIZATION DOMAIN, 2 INTRACELLULAR GATE, TETRAMER
1528	1tld	A	117	204	1.3e-11	0.26	0.45		POTASSIUM CHANNEL KVL1.1; CHAIN: A;	PROTON TRANSPORT POTASSIUM CHANNELS, TETRAMERIZATION DOMAIN, X-RAY STRUCTURE, 2 APLYSIA KV1.1, PROTON TRANSPORT
1528	3kvt		117	217	6e-15	0.59	0.62		POTASSIUM CHANNEL PROTEIN SHAW; CHAIN: NULL;	POTASSIUM CHANNEL POTASSIUM CHANNEL, TETRAMERIZATION DOMAIN, MOLECULAR 2 RECOGNITION, ZINC-BINDING
1529	1a12	A	346	704	1.7e-49	0.04	-0.08		REGULATOR OF CHROMOSOME CONDENSATION 1; CHAIN: A, B, C;	GUANINE NUCLEOTIDE EXCHANGE FACTOR RCC1; GUANINE NUCLEOTIDE EXCHANGE FACTOR, GEF, RAN, 2 RAS-LIKE NUCLEAR GTP BINDING PROTEIN HEADER TER
1529	1a12	A	354	741	1.7e-49			97.41	REGULATOR OF CHROMOSOME CONDENSATION 1; CHAIN: A, B, C;	GUANINE NUCLEOTIDE EXCHANGE FACTOR RCC1; GUANINE NUCLEOTIDE EXCHANGE FACTOR, GEF, RAN, 2 RAS-LIKE NUCLEAR GTP BINDING PROTEIN HEADER TER
1529	1a12	A	9	415	6.8e-91	-0.01	0.22		REGULATOR OF CHROMOSOME CONDENSATION 1; CHAIN: A, B, C;	GUANINE NUCLEOTIDE EXCHANGE FACTOR RCC1; GUANINE NUCLEOTIDE EXCHANGE FACTOR, GEF, RAN, 2 RAS-LIKE NUCLEAR GTP BINDING PROTEIN HEADER TER
1529	1dbh	A	695	1001	3e-16	-0.03	0.22		HUMAN SOS 1; CHAIN: A;	GENE REGULATION SON OF SEVENLESS PROTEIN; GUANINE

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										NUCLEOTIDE EXCHANGE FACTOR, GENE REGULATION
1529	1fao	A	930	1006	7.5e-07	-0.27	0.33		DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3-CHAIN: A;	SIGNALING PROTEIN DAPP1, PHISH, BAM32; PLECKSTRIN, 3-PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN
1529	1fb8	A	930	1007	3e-07	0.02	0.35		DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3-CHAIN: A;	SIGNALING PROTEIN DAPP1, PHISH, BAM32; PLECKSTRIN, 3-PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN
1529	1pls		935	1007	0.0003	0.38	0.93		PHOSPHORYLATION PLECKSTRIN (N-TERMINAL PLECKSTRIN HOMOLOG DOMAIN) MUTANT 1PLS 3 WITH LEU GLU (HIS)6 ADDED TO THE C TERMINUS 1PLS 4 (INS(G105-LEHHHHH)) (NMR, 25 STRUCTURES) 1PLS 5	
1529	1pms		897	1004	1.5e-09	0.32	-0.02		SOS 1; CHAIN: NULL;	SIGNAL TRANSDUCTION SON OF SEVENLESS; PLECKSTRIN, SON OF SEVENLESS, SIGNAL TRANSDUCTION
1530	1dlj	A	2	138	6.8e-52	1.32	1.00		PROFILIN II; CHAIN: A, B, C, D;	CONTRACTILE PROTEIN ACIDIC PROFILIN ISOFORM, ACTIN-BINDING PROTEIN, POLY-L-2 PROLINE BINDING PROTEIN, CONTRACTILE PROTEIN
1530	1dlj	A	2	138	9e-63	1.32	1.00		PROFILIN II; CHAIN: A, B, C, D;	CONTRACTILE PROTEIN ACIDIC PROFILIN ISOFORM, ACTIN-

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1530	1fil		2	140	1.7e-52	1.04	1.00		PROFILIN; CHAIN: NULL;	BINDING PROTEIN, POLY-L-2 PROLINE BINDING PROTEIN, CONTRACTILE PROTEIN
1530	1fil		2	140	1.7e-52			167.69	PROFILIN; CHAIN: NULL;	PROTEIN BINDING ACETYLATION, ACTIN-BINDING PROTEIN, MULTIGENE FAMILY
1530	1pne		2	140	1.7e-52	0.92	1.00		ACTIN BINDING PROTEIN PROFILIN 1PNE 3	PROTEIN BINDING ACETYLATION, ACTIN-BINDING PROTEIN, MULTIGENE FAMILY
1530	1pne		2	140	1.7e-52			167.40	ACTIN BINDING PROTEIN PROFILIN 1PNE 3	
1531	1d1j	A	2	122	1.7e-42	0.75	1.00		PROFILIN II; CHAIN: A, B, C, D;	CONTRACTILE PROTEIN ACIDIC PROFILIN ISOFORM, ACTIN-BINDING PROTEIN, POLY-L-2 PROLINE BINDING PROTEIN, CONTRACTILE PROTEIN
1531	1d1j	A	2	122	4.5e-52	0.71	1.00		PROFILIN II; CHAIN: A, B, C, D;	CONTRACTILE PROTEIN ACIDIC PROFILIN ISOFORM, ACTIN-BINDING PROTEIN, POLY-L-2 PROLINE BINDING PROTEIN, CONTRACTILE PROTEIN
1531	1pne		2	124	1.5e-42	0.64	1.00		ACTIN BINDING PROTEIN PROFILIN 1PNE 3	
1531	1pne		2	124	1.5e-42			133.14	ACTIN BINDING PROTEIN PROFILIN 1PNE 3	
1534	1bg2		2	176	3e-68	-0.22	1.00		KINESIN; CHAIN: NULL;	MOTOR PROTEIN MOTOR PROTEIN, ATPASE, MICROTUBULE ASSOCIATED
1534	1bg2		2	176	6.8e-35	-0.15	1.00		KINESIN; CHAIN: NULL;	MOTOR PROTEIN MOTOR PROTEIN, ATPASE, MICROTUBULE

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Coumpound	PDB annotation
1534	1cz7	A	4	170	1e-17	-0.36	0.10		MICROTUBULE MOTOR PROTEIN NCD; CHAIN: A, B, C, D;	ASSOCIATED CONTRACTILE PROTEIN NCD, CLARET SEGREGATIONAL PROTEIN; NCD CRYSTAL STRUCTURE, MICROTUBULE MOTORS, KINESIN 2 SUPERFAMILY, CONTRACTILE PROTEIN MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1534	2kin	B	101	186	3e-40	0.03	0.83		KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1534	2kin	B	101	199	6.8e-19	-0.17	1.00		KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1534	2ncd	A	4	170	6.8e-18	-0.24	0.54		KINESIN MOTOR NCD; CHAIN: A;	CONTRACTILE PROTEIN KINESIN, MICROTUBULE-BASED MOTOR, NCD, CONTRACTILE PROTEIN
1534	3kar		1	172	1.7e-21	-0.30	0.66		KINESIN-LIKE PROTEIN KAR3; CHAIN: NULL;	CONTRACTILE PROTEIN CONTRACTILE PROTEIN, KAR3, KINESIN-RELATED PROTEIN, MOTOR 2 PROTEIN, ATPASE, P-LOOP, MICROTUBULE BINDING PROTEIN
1534	3kin	B	105	186	1.5e-38	-0.25	0.98		KINESIN HEAVY CHAIN; CHAIN: A, B, C, D;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1534	3kin	B	105	230	1.7e-20	-0.44	0.71		KINESIN HEAVY CHAIN; CHAIN: A, B, C, D;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1536	1ars		71	369	6.8e-13	-0.22	0.07		TRANSFERASE(AMINOTRANSFERASE) ASPARTATE AMINOTRANSFERASE (E.C.2.6.1.1) COMPLEXED WITH 1ARS 3 PYRIDOXAL-5'-PHOSPHATE 1ARS 4	
1536	1bjw	A	1	369	5.1e-81	0.17	0.75		ASPARTATE AMINOTRANSFERASE; CHAIN: A, B;	AMINOTRANSFERASE AMINOTRANSFERASE, PYRIDOXAL ENZYME

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQPOLD score	Compound	PDB annotation
1536	1bs0	A	1	375	1.7e-41			69.72	8-AMINO-7-OXONANOATE SYNTHASE; CHAIN: A;	TRANSFERASE AONS, 8-AMINO-7-KETOPELARGONATE SYNTHASE; PLP-DEPENDENT ACYL-COA SYNTHASE, BIOTIN BIOSYNTHESIS, 8-2 AMINO-7-OXONANOATE SYNTHASE, 8-AMINO-7-KETOPELARGONATE 3 SYNTHASE, TRANSFERASE
1536	1bs0	A	47	365	1.7e-41	0.32	0.12		8-AMINO-7-OXONANOATE SYNTHASE; CHAIN: A;	TRANSFERASE AONS, 8-AMINO-7-KETOPELARGONATE SYNTHASE; PLP-DEPENDENT ACYL-COA SYNTHASE, BIOTIN BIOSYNTHESIS, 8-2 AMINO-7-OXONANOATE SYNTHASE, 8-AMINO-7-KETOPELARGONATE 3 SYNTHASE, TRANSFERASE
1536	1bw0	A	1	373	6.8e-54	0.09	0.16		TYROSINE AMINOTRANSFERASE; CHAIN: A, B;	TRANSFERASE TAT; TYROSINE CATABOLISM, TRANSFERASE, AMINOTRANSFERASE, 2 PYRIDOXAL-5'-PHOSPHATE, PLP
1536	1c7n	A	68	373	1.7e-18	-0.03	0.25		CYSTALYSIN; CHAIN: A, B, C, D, E, F, G, H;	TRANSFERASE TRANSFERASE, AMINOTRANSFERASE, PYRIDOXAL PHOSPHATE
1536	1d2f	A	92	373	3.4e-21	0.10	-0.05		MALY PROTEIN; CHAIN: A, B;	TRANSFERASE AMINOTRANSFERASE FOLD, LARGE PLP-BINDING DOMAIN, SMALL C-2 TERMINAL DOMAIN, OPEN ALPHA-BETA STRUCTURE.
1536	1d7u	A	1	372	3.4e-63			169.86	2,2-DIALKYLGLYCINE DECARBOXYLASE (PYRUVATE); CHAIN: A;	LYASE DGD; ENZYME COMPLEXES, CATALYTIC MECHANISM, DECARBOXYLATION 2 INHIBITOR, LYASE
1536	1d7u	A	46	372	3.4e-63	0.72	1.00		2,2-DIALKYLGLYCINE DECARBOXYLASE	LYASE DGD; ENZYME COMPLEXES, CATALYTIC MECHANISM,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									(PYRUVATE); CHAIN: A;	DECARBOXYLATION 2 INHIBITOR, LYASE
1536	1gtx	A	49	370	1.5e-70	0.71	1.00		4-AMINO BUTYRATE AMINOTRANSFERASE; CHAIN: A, B, C, D;	TRANSFERASE GABA-AT; PLP-DEPENDENT ENZYME, AMINOTRANSFERASE, 4-AMINO BUTYRIC ACID, 2 ANTIEPILEPTIC DRUG TARGET
1536	1gtx	A	53	373	1.7e-53	0.47	1.00		4-AMINO BUTYRATE AMINOTRANSFERASE; CHAIN: A, B, C, D;	TRANSFERASE GABA-AT; PLP-DEPENDENT ENZYME, AMINOTRANSFERASE, 4-AMINO BUTYRIC ACID, 2 ANTIEPILEPTIC DRUG TARGET
1536	1ql5	A	40	371	6.8e-64	0.54	1.00		7,8-DIAMINOPELARGONIC ACID SYNTHASE; CHAIN: A, B;	AMINOTRANSFERASE AMINOTRANSFERASE, PYRIDOXAL-5'-PHOSPHATE, BIOTIN 2 BIOSYNTHESIS
1536	2gsa	A	1	372	1.2e-72			90.43	GLUTAMATE SEMIALDEHYDE AMINOTRANSFERASE; CHAIN: A, B;	CHLOROPHYLL BIOSYNTHESIS GLUTAMATE SEMIALDEHYDE AMINOMUTASE; CHLOROPHYLL BIOSYNTHESIS, PYRIDOXAL-5'-PHOSPHATE, 2 PYRIDOXAMINE-5'-PHOSPHATE, ASYMMETRIC DIMER
1536	2gsa	A	5	372	1.2e-72	0.25	1.00		GLUTAMATE SEMIALDEHYDE AMINOTRANSFERASE; CHAIN: A, B;	CHLOROPHYLL BIOSYNTHESIS GLUTAMATE SEMIALDEHYDE AMINOMUTASE; CHLOROPHYLL BIOSYNTHESIS, PYRIDOXAL-5'-PHOSPHATE, 2 PYRIDOXAMINE-5'-PHOSPHATE, ASYMMETRIC DIMER
1536	2oat	A	2	372	1.7e-62			130.71	ORNITHINE AMINOTRANSFERASE; CHAIN: A, B, C;	AMINOTRANSFERASE AMINOTRANSFERASE, 5-FLUOROMETHYLORNITHINE, PLP-DEPENDENT 2 ENZYME, PYRIDOXAL PHOSPHATE
1536	2oat	A	40	369	1.7e-62	0.57	1.00		ORNITHINE	AMINOTRANSFERASE

SEQ ID NO:	PDB ID	CHAIN N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									AMINOTRANSFERASE; CHAIN: A, B, C;	AMINOTRANSFERASE, 5-FLUOROMETHYLORNITHINE, PLP-DEPENDENT 2 ENZYME, PYRIDOXAL PHOSPHATE
1539	1eul	A	91	916	0	-0.16	0.04		CALCIUM-TRANSPORTING ATPASE SARCOPLASMIC CHAIN: A;	HYDROLASE SERCA1; ION PUMP, CALCIUM, MEMBRANE PROTEIN, P-TYPE ATPASE, ACTIVE 2 TRANSPORT
1541	1a17		135	247	3.4e-23	0.06	0.77		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
1541	1a17		179	253	1e-10	-0.35	0.15		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
1541	1e96	B	102	230	1.5e-13	-0.12	0.29		RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	SIGNALLING COMPLEX RAC1; P67PHOX; SIGNALLING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF
1541	1elr	A	101	196	1e-12	0.21	0.54		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1541	1elr	A	139	231	1e-18	0.00	0.19		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1541	1elr	A	67	167	1e-18	0.26	0.52		TPR2A-DOMAIN OF HOP;	CHAPERONE HOP, TPR-DOMAIN,

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1541	1elw	A	133	250	1.7e-20	-0.04	0.53		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1541	1elw	A	28	133	3.4e-15	0.30	0.01		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1541	1elw	A	64	175	1e-14	0.73	0.46		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1541	1elw	A	98	202	3.4e-13	0.35	0.37		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1541	1feh	A	6	252	8.5e-35	-0.06	0.18		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOME RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
1541	1qge	A	2	254	3.4e-07			63.04	VESICULAR TRANSPORT PROTEIN SEC17; CHAIN: A;	PROTEIN TRANSPORT HELIX-TURN-HELIX TPR-LIKE REPEAT, PROTEIN TRANSPORT
1542	1d2h	A	65	190	3.4e-16	0.55	-0.09		GLYCINE N-METHYLTRANSFERASE; CHAIN: A, B, C, D;	TRANSFERASE METHYLTRANSFERASE
1542	1dus	A	72	187	3.4e-09	0.57	0.37		MJ0882; CHAIN: A;	STRUCTURAL GENOMICS HYPOTHETICAL PROTEIN,

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1542	1qam	A	72	200	3e-06	0.27	0.00		ERMIC METHYLTRANSFERASE; CHAIN: A;	METHANOCOCCUS JANNASCHII TRANSFERASE RRNA METHYLTRANSFERASE ERMIC, COFACTOR ANALOGS
1542	1xva	A	21	190	3.4e-17	-0.00	-0.13		GLYCINE N- METHYLTRANSFERASE; CHAIN: A, B;	METHYLTRANSFERASE GNMT, S- ADENOSYL-L-METHIONINE; GLYCINE METHYLTRANSFERASE
1542	2adim	A	66	192	5.1e-11	0.14	-0.14		ADENINE-N6-DNA- METHYLTRANSFERASE TAQI; CHAIN: A, B;	METHYLTRANSFERASE TRANSFERASE, METHYLTRANSFERASE, RESTRICTION SYSTEM
1542	2adim	A	66	337	7.5e-06	-0.29	0.16		ADENINE-N6-DNA- METHYLTRANSFERASE TAQI; CHAIN: A, B;	METHYLTRANSFERASE TRANSFERASE, METHYLTRANSFERASE, RESTRICTION SYSTEM
1544	1a17		1	58	1.5e-06	-0.10	0.28		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRIPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
1544	1feh	A	2	83	4.5e-06	0.17	0.25		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOMERE RECEPTOR 1, PTS1- BP, PEROXIN-5, PTS1 PROTEIN- PEPTIDE COMPLEX, TETRATRIPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
1545	1ahd	P	228	291	5.1e-32			58.51	DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 1AHD 3 REPLACED BY SER (C39S) COMPLEX WITH DNA (NMR,	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									1AHD 4 16 STRUCTURES) 1AHD 5	
1545	1ahd	P	229	294	5.1e-32	0.01	1.00		DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 1AHD 3 REPLACED BY SER (C39S) COMPLEX WITH DNA (NMR, 1AHD 4 16 STRUCTURES) 1AHD 5	
1545	1au7	A	212	286	4.5e-22	-0.40	0.59		PIT-1; CHAIN: A, B; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) GHF-1; COMPLEX (DNA-BINDING PROTEIN/DNA), PITUITARY, CPD, 2 POU DOMAIN, TRANSCRIPTION FACTOR
1545	1b72	A	224	290	3e-28			78.21	HOMEODOMAIN PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA CHAIN: D; DNA CHAIN: E;	PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA
1545	1b72	A	233	290	3e-28	0.40	1.00		HOMEODOMAIN PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA CHAIN: D; DNA CHAIN: E;	PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA
1545	1b72	A	233	290	5.1e-26	0.40	1.00		HOMEODOMAIN PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA CHAIN: D; DNA CHAIN: E;	PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA
1545	1b8i	A	226	287	5.1e-27			55.32	ULTRABITHORAX HOMEOTIC PROTEIN IV; CHAIN: A; HOMEODOMAIN PROTEIN EXTRADENTICLE; CHAIN: B; DNA (5'- CHAIN: C; DNA (5'- CHAIN: D;	TRANSCRIPTION/DNA ULTRABITHORAX; PBX PROTEIN; DNA BINDING, HOMEODOMAIN, HOMEOTIC PROTEINS, DEVELOPMENT, 2 SPECIFICITY
1545	1b8i	A	233	287	5.1e-27	0.49	1.00		ULTRABITHORAX HOMEOTIC PROTEIN IV; CHAIN: A; HOMEODOMAIN PROTEIN EXTRADENTICLE; CHAIN: B;	TRANSCRIPTION/DNA ULTRABITHORAX; PBX PROTEIN; DNA BINDING, HOMEODOMAIN, HOMEOTIC PROTEINS,

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									DNA (5'- CHAIN: C; DNA (5'- CHAIN: D;	DEVELOPMENT, 2 SPECIFICITY
1545	1ftz		227	296	8.5e-28			59.53	DNA-BINDING FUSHI TARAZU PROTEIN (HOMEODOMAIN) (NMR, 20 STRUCTURES) IFTZ 3	
1545	1ftz		229	294	8.5e-28	-0.12	0.92		DNA-BINDING FUSHI TARAZU PROTEIN (HOMEODOMAIN) (NMR, 20 STRUCTURES) IFTZ 3	
1545	1san		234	291	1.4e-29			57.26	DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 ISAN 3 REPLACED BY SER AND RESIDUES 1-6 DELETED (C39S,DEL 1-6) ISAN 4 (NMR, 20 STRUCTURES) ISAN 5	
1545	1san		235	294	1.4e-29	0.30	1.00		DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 ISAN 3 REPLACED BY SER AND RESIDUES 1-6 DELETED (C39S,DEL 1-6) ISAN 4 (NMR, 20 STRUCTURES) ISAN 5	
1545	9ant	A	233	288	1.7e-29	0.42	1.00		ANTENNAPEDIA PROTEIN; CHAIN: A, B; DNA; CHAIN: C, D, E, F;	COMPLEX (DNA-BINDING PROTEIN/DNA) HD; HOMEODOMAIN, COMPLEX (DNA-BINDING PROTEIN/DNA)
1545	9ant	A	233	288	1.7e-29			61.44	ANTENNAPEDIA PROTEIN; CHAIN: A, B; DNA; CHAIN: C, D, E, F;	COMPLEX (DNA-BINDING PROTEIN/DNA) HD; HOMEODOMAIN, COMPLEX (DNA-BINDING PROTEIN/DNA)
1546	1alh	A	12	92	1.4e-27	0.19	1.00		QGSR ZINC FINGER PEPTIDE;	COMPLEX (ZINC FINGER/DNA)

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1546	1alh	A	161	249	8.5e-27	0.26	1.00		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA), COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1546	1alh	A	162	250	3e-28	0.16	0.88		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA), COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1546	1alh	A	199	277	1.5e-37	0.48	1.00		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA), COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1546	1alh	A	1	64	5.1e-22	0.31	0.80		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA), COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1546	1alh	A	281	361	3.4e-30	0.22	1.00		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA), COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1546	1alh	A	309	391	3.4e-30			80.58	QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA), COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1546	1mey	C	101	185	1.5e-14	0.01	0.23		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1546	1mey	C	11	92	1e-46	0.48	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1546	1mey	C	125	249	6e-25	-0.12	0.49		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1546	1mey	C	130	221	1.5e-39	-0.10	0.48		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1546	1mey	C	160	249	5.1e-47	0.09	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1546	1mey	C	188	277	1.7e-47	0.57	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1546	1mey	C	1	64	5.1e-34	0.26	0.95		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1546	1mey	C	224	305	1e-49	0.81	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1546	1mey	C	224	306	1e-49			105.23	DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1546	1mey	C	252	333	1.2e-49	0.59	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1546	1mey	C	280	361	3.4e-49	0.38	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1546	1mey	C	308	389	1.2e-49	0.37	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1546	1mey	C	336	411	3.4e-44	0.26	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1546	1tf6	A	132	291	1.4e-31	0.03	0.46		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1546	1tf6	A	196	359	1.5e-37			117.50	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1546	1tf6	A	199	342	1.5e-37	0.41	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1546	1tf6	A	253	403	1.5e-37	0.32	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1546	1tf6	A	309	410	1.7e-26	0.07	0.75		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1546	1ubd	C	133	249	6.8e-31	0.20	0.96		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1546	1ubd	C	165	277	3e-40	0.28	0.99		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA)

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1546	1ubd	C	168	277	5.1e-33	0.47	1.00		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1546	1ubd	C	16	119	3e-25	0.24	0.81		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1546	1ubd	C	19	150	1.7e-23	-0.28	0.16		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1546	1ubd	C	1	92	3.4e-29	-0.01	1.00		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									CHAIN: A, B;	INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1546	1ubd	C	201	333	7.5e-48	0.25	1.00		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1546	1ubd	C	226	334	1.2e-50			97.53	YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1546	1ubd	C	250	362	1.2e-50	0.44	1.00		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1546	1ubd	C	279	389	4.5e-47	0.42	1.00		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1546	1ubd	C	288	389	1.7e-33	0.35	1.00		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1546	1ubd	C	306	417	7.5e-46	0.11	1.00		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1546	1ubd	C	316	410	8.5e-32	0.16	0.93		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1546	2drp	A	63	122	1e-10	0.24	0.74		COMPLEX(TRANSCRIPTION REGULATION/DNA) TRAMTRACK PROTEIN (TWO ZINC-FINGER PEPTIDE) COMPLEXED WITH 2DRP 3 DNA 2DRP 4	
1546	2gli	A	12	150	6e-32	0.09	0.68		ZINC FINGER PROTEIN GLI1;	COMPLEX (DNA-BINDING)

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									CHAIN: A; DNA; CHAIN: C, D;	PROTEIN/DNA FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1546	2gli	A	137	248	3.4e-26	-0.08	0.34		ZINC FINGER PROTEIN GLI; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1546	2gli	A	160	304	3.4e-32	0.34	0.94		ZINC FINGER PROTEIN GLI; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1546	2gli	A	224	363	1.2e-63			106.53	ZINC FINGER PROTEIN GLI; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1546	2gli	A	224	391	1.2e-63	0.35	1.00		ZINC FINGER PROTEIN GLI; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1546	2gli	A	260	388	3.4e-34	0.40	0.95		ZINC FINGER PROTEIN GLI; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1546	2gli	A	280	418	9e-45	0.13	1.00		ZINC FINGER PROTEIN GLI; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1546	2gli	A	288	410	6.8e-31	0.45	1.00		ZINC FINGER PROTEIN GLI; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1546	2gli	A	99	279	1.5e-42	0.14	0.99		ZINC FINGER PROTEIN GLI; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										BINDING PROTEIN/DNA)
1547	1f1g	E	217	366	1e-53	0.78	1.00		16S RIBOSOMAL RNA; CHAIN: A; FRAGMENT OF MESSENGER RNA; CHAIN: X; 30S RIBOSOMAL PROTEIN S2; CHAIN: B; 30S RIBOSOMAL PROTEIN S3; CHAIN: C; 30S RIBOSOMAL PROTEIN S4; CHAIN: D; 30S RIBOSOMAL PROTEIN S5; CHAIN: E; 30S RIBOSOMAL PROTEIN S6; CHAIN: F; 30S RIBOSOMAL PROTEIN S7; CHAIN: G; 30S RIBOSOMAL PROTEIN S8; CHAIN: H; 30S RIBOSOMAL PROTEIN S9; CHAIN: I; 30S RIBOSOMAL PROTEIN S10; CHAIN: J; 30S RIBOSOMAL PROTEIN S11; CHAIN: K; 30S RIBOSOMAL PROTEIN S12; CHAIN: L; 30S RIBOSOMAL PROTEIN S13; CHAIN: M; 30S RIBOSOMAL PROTEIN S14; CHAIN: N; 30S RIBOSOMAL PROTEIN S15; CHAIN: O; 30S RIBOSOMAL PROTEIN S16; CHAIN: P; 30S RIBOSOMAL PROTEIN S17; CHAIN: Q; 30S RIBOSOMAL PROTEIN S18; CHAIN: R; 30S RIBOSOMAL PROTEIN S19; CHAIN: S; 30S RIBOSOMAL PROTEIN S20; CHAIN: T; 30S RIBOSOMAL PROTEIN THX; CHAIN: V	RIBOSOME 30S RIBOSOMAL SUBUNIT, RIBOSOME, ANTIBIOTIC, STREPTOMYCIN, 2 SPECTINOMYCIN, PAROMOMYCIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1547	1pkp		211	357	1e-56			64.28	RIBOSOMAL PROTEIN S5 (PROKARYOTIC) 1PKP 3	
1547	1pkp		217	357	1e-56	0.53	1.00		RIBOSOMAL PROTEIN S5 (PROKARYOTIC) 1PKP 3	
1549	1erj	A	119	219	0.0045	0.31	0.11		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
1553	1mey	C	172	251	5.1e-29	0.02	-0.20		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1553	1mey	C	77	169	5.1e-33	-0.41	0.09		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1553	1mey	G	77	104	1.7e-07	-0.05	0.18		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1553	1sp2		173	203	1.7e-10	0.21	-0.20		SP1F2; CHAIN: NULL;	ZINC FINGER TRANSCRIPTION FACTOR SP1; ZINC FINGER, TRANSCRIPTION ACTIVATION, SP1
1553	1sp2		78	108	8.5e-09	0.05	-0.13		SP1F2; CHAIN: NULL;	ZINC FINGER TRANSCRIPTION FACTOR SP1; ZINC FINGER, TRANSCRIPTION ACTIVATION, SP1
1553	1tf3	A	69	130	1.7e-15	-0.63	0.07		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									CHAIN: E, F;	GENE; NMR, TFIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
1553	1ubd	C	49	130	1.4e-15	-0.83	0.24		YY1; CHAIN: C; ADENOVIRUS ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1553	1zfd		78	104	5.1e-06	-0.36	0.00		SW15; CHAIN: NULL;	ZINC FINGER DNA BINDING DOMAIN DNA BINDING MOTIF, ZINC FINGER DNA BINDING DOMAIN
1553	2drp	A	74	130	1.7e-06	0.04	0.36		COMPLEX(TRANSCRIPTION REGULATION/DNA) TRAMTRACK PROTEIN (TWO ZINC-FINGER PEPTIDE) COMPLEXED WITH 2DRP 3 DNA 2DRP 4	
1553	2gli	A	52	201	3.4e-41	-0.30	0.03		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1553	2gli	A	79	229	3.4e-41			54.61	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1554	1fs1	A	8	47	4.5e-07	-0.10	0.41		CYCLIN A/CDK2-ASSOCIATED	LIGASE SKP2 F-BOX; SKP1; SKP1,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
									P19; CHAIN: A, C; CYCLIN A/CDK2-ASSOCIATED P45; CHAIN: B, D;	SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1558	1jkw		1	66	3e-11	-0.49	0.24		CYCLIN H; CHAIN: NULL;	CELL DIVISION CYCLIN H (RECOMBINANT); CYCLIN, CELL CYCLE, CELL DIVISION, NUCLEAR PROTEIN
1558	1qmz	B	5	62	1.5e-09	-0.36	0.28		CELL DIVISION PROTEIN KINASE 2; CHAIN: A, C; G2/MITOTIC-SPECIFIC CYCLIN A; CHAIN: B, D; SUBSTRATE PEPTIDE; CHAIN: E, F;	COMPLEX (PROTEIN KINASE/CYCLIN) CYCLIN-DEPENDENT KINASE-2, CDK2, P33 PROTEIN KINASE; CCNA, CCNI; COMPLEX (PROTEIN KINASE/CYCLIN), CYCLIN, CDK, 2 PHOSPHORYLATION, SUBSTRATE COMPLEX
1559	1aip	A	122	541	0	0.02	0.78		ELONGATION FACTOR TU; CHAIN: A, B, E, F; ELONGATION FACTOR TS; CHAIN: C, D, G, H;	COMPLEX OF TWO ELONGATION FACTORS EF-TU; EF-TS; ELONGATION FACTOR, NUCLEOTIDE EXCHANGE, GTP-BINDING, 2 COMPLEX OF TWO ELONGATION FACTORS
1559	1aip	A	165	542	0			134.70	ELONGATION FACTOR TU; CHAIN: A, B, E, F; ELONGATION FACTOR TS; CHAIN: C, D, G, H;	COMPLEX OF TWO ELONGATION FACTORS EF-TU; EF-TS; ELONGATION FACTOR, NUCLEOTIDE EXCHANGE, GTP-BINDING, 2 COMPLEX OF TWO ELONGATION FACTORS
1559	1d2e	A	122	548	0	0.41	1.00		ELONGATION FACTOR TU (EF-TU); CHAIN: A, B, C, D	RNA BINDING PROTEIN G-PROTEIN, BETA-BARREL
1559	1d2e	A	124	552	0			131.00	ELONGATION FACTOR TU (EF-TU); CHAIN: A, B, C, D	RNA BINDING PROTEIN G-PROTEIN, BETA-BARREL
1559	1efc	A	121	541	0	0.47	1.00		ELONGATION FACTOR;	RNA BINDING PROTEIN EF-TU;

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: A, B;	TRANSPORT AND PROTECTION PROTEIN, RNA BINDING PROTEIN
1559	1efc	A	137	542	0			129.64	ELONGATION FACTOR; CHAIN: A, B;	RNA BINDING PROTEIN EFTU; TRANSPORT AND PROTECTION PROTEIN, RNA BINDING PROTEIN
1559	1efu	A	122	541	0	-0.05	0.86		ELONGATION FACTOR TU; CHAIN: A, C; ELONGATION FACTOR TS; CHAIN: B, D;	COMPLEX (TWO ELONGATION FACTORS) ELONGATION FACTOR FOR TRANSFER, HEAT UNSTABLE, ELONGATION FACTOR FOR TRANSFER, HEAT STABLE, ELONGATION FACTOR, COMPLEX (TWO ELONGATION FACTORS)
1559	1efu	A	172	542	0			115.68	ELONGATION FACTOR TU; CHAIN: A, C; ELONGATION FACTOR TS; CHAIN: B, D;	COMPLEX (TWO ELONGATION FACTORS) ELONGATION FACTOR FOR TRANSFER, HEAT UNSTABLE, ELONGATION FACTOR FOR TRANSFER, HEAT STABLE, ELONGATION FACTOR, COMPLEX (TWO ELONGATION FACTORS)
1559	1ega	A	126	368	1.5e-13	0.05	0.13		GTP-BINDING PROTEIN ERA; CHAIN: A, B;	HYDROLASE ERA, GTPASE, RNA-BINDING, RAS-LIKE, HYDROLASE
1559	1etu		118	345	8.5e-67	0.18	0.45		TRANSPORT AND PROTECTION PROTEIN ELONGATION FACTOR TU (DOMAIN I) - *GUANOSINE DIPHOSPHATE IETU 4 COMPLEX IETU 5	
1559	1exm	A	117	541	0	0.29	1.00		ELONGATION FACTOR TU (EF-TU); CHAIN: A;	TRANSLATION EF-TU; GTPASE, MOLECULAR SWITCH, TRNA, RIBOSOME, Q-BETA REPLICASE, 2 CHAPERONE, DISULFIDE ISOMERASE
1559	1f60	A	120	542	0	0.31	1.00		ELONGATION FACTOR EEF1A; CHAIN: A; ELONGATION	TRANSLATION PROTEIN-PROTEIN COMPLEX

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1559	1fnn	A	319	459	1.7e-05	-0.15	0.00		FACTOR EEF1B; CHAIN: B; ELONGATION FACTOR G; CHAIN: A;	TRANSLATION EF-G; BENT CONFORMATION, VISIBLE DOMAIN III, MUTATION HIS573ALA
1559	1g7s	A	123	553	8.5e-62	0.03	0.28		TRANSLATION INITIATION FACTOR IF2/EIF5B; CHAIN: A;	TRANSLATION TRANSLATIONAL GTPASE
1561	1a17		19	165	4.5e-09	0.08	0.07		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
1561	1a17		2	105	1.2e-06	-0.01	0.83		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
1561	1elr	A	19	111	1.3e-08	0.01	0.70		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1561	1elr	A	316	401	0.0012	-0.46	0.03		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1561	1elr	A	462	558	0.003	-0.07	0.10		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1561	1elr	A	54	119	0.0003	0.36	0.41		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1561	1elr	A	63	165	0.0001	-0.02	0.05		TPR2A-DOMAIN OF HOP;	CHAPERONE HOP, TPR-DOMAIN, BINDING

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1561	1elw	A	19	119	7.5e-08	0.38	0.98		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1561	1elw	A	25	123	5.1e-06	0.26	0.71		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1561	1elw	A	2	97	4.5e-07	0.31	0.95		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1561	1elw	A	382	472	0.00034	-0.68	0.19		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1561	1elw	A	458	537	1.7e-05	0.41	0.12		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1561	1fch	A	17	252	1.3e-13	0.25	0.65		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOMORE RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
1561	1fch	A	2	119	1.2e-10	0.34	0.31		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOMORE RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1561	1feh	A	318	563	3.4e-10	0.05	0.03		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	2 HELICAL REPEAT SIGNALING PROTEIN PEROXISOMORE RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
1561	1feh	A	31	286	1.4e-11	0.10	0.48		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOMORE RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
1563	1av1	A	41	242	1.4e-07			68.91	APOLIPOPROTEIN A-I; CHAIN: A, B, C, D;	LIPID TRANSPORT APO A-I; LIPOPROTEIN, LIPID TRANSPORT, CHOLESTEROL METABOLISM, 2 ATHEROSCLEROSIS, HDL, LCAT-ACTIVATION
1563	1cun	A	19	233	1.5e-10			68.37	ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1563	1cun	A	61	269	1.5e-10	0.04	0.03		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1563	1dn1	B	18	254	1.5e-13	-0.33	0.10		SYNTAXIN BINDING PROTEIN I; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
1563	1ez3	A	5	128	1.5e-07	0.19	0.00		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
										KDA PROTEIN, P35A, THREE HELIX BUNDLE
1563	1qqe	A	2	283	1.2e-09			66.08	VESICULAR TRANSPORT PROTEIN SEC17; CHAIN: A;	PROTEIN TRANSPORT HELIX-TURN-HELIX TPR-LIKE REPEAT, PROTEIN TRANSPORT
1563	1quu	A	22	291	4.5e-17			71.18	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
1563	1quu	A	5	246	4.5e-17	0.01	-0.06		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
1563	1sig		92	287	1.2e-06	0.09	0.12		RNA POLYMERASE PRIMARY SIGMA FACTOR; CHAIN: NULL;	TRANSCRIPTION REGULATION SIGMA70; RNA POLYMERASE SIGMA FACTOR, TRANSCRIPTION REGULATION
1565	1a4y	A	11	143	1e-13	0.06	0.00		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS
1565	1a4y	A	3	176	1.5e-13	0.50	0.62		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS
1565	1fo1	B	43	133	6.8e-09	0.04	-0.05		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1565	1fqv	A	3	140	3.4e-15	0.06	0.01		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45; CYCLIN

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									N, P;	A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1565	1fqv	A	3	174	3e-17	0.74	0.99		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1565	1fs2	A	3	140	3.4e-15	0.23	0.07		SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	LIGASE CYCLIN A/CDK2-ASSOCIATED P45; CYCLIN A/CDK2-ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
1565	2bnh		11	143	1.5e-12	0.01	0.03		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLTATION, LEUCINE-RICH REPEATS
1565	2bnh		2	176	4.5e-10	0.18	0.35		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLTATION, LEUCINE-RICH REPEATS
1567	2cba		3	242	0	1.12	1.00		LYASE(OXO-ACID) CARBONIC ANHYDRASE II (E.C.4.2.1.1) (50 MM TRIS, 2CBA 3 M AMMONIUM SULFATE, PH 7.8) 2CBA 4	
1567	2cba		3	242	0			403.66	LYASE(OXO-ACID) CARBONIC ANHYDRASE II (E.C.4.2.1.1) (50 MM TRIS, 2CBA 3 M AMMONIUM SULFATE, PH 7.8)	